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OM nucleic - nucleic search, using SW model
Run on: December 27, 2005, 14:44:36 ; Search time 146 Seconds

413.953 Million cell updates/sec

Title: US-10-812-642-115
Perfect score: 34
Sequence: 1 ggagguauuacagacguuguauagcugacucc 34

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Issued Patents NA:
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5: /cgn2_6/ptodata/1/ina/H_COMB.seq: *
6: /cgn2_6/ptodata/1/ina/PCTRUS_COMB.seq: *
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8: /cgn2_6/ptodata/1/ina/RE_COMB.seq: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	34	3 US-09-363-939A-93	Sequence 93, App1
2	34	100.0	34	3 US-09-363-939A-115	Sequence 115, App
3	34	100.0	34	3 US-09-363-939A-121	Sequence 121, App
4	34	100.0	34	3 US-09-363-939A-171	Sequence 171, App
5	34	100.0	34	3 US-09-363-939A-172	Sequence 172, App
6	34	100.0	34	3 US-09-363-939A-173	Sequence 173, App
7	34	100.0	34	3 US-09-363-939A-174	Sequence 174, App
8	34	100.0	34	3 US-09-363-939A-175	Sequence 175, App
9	34	100.0	34	3 US-09-363-939A-176	Sequence 176, App
10	34	100.0	34	3 US-09-363-939A-177	Sequence 177, App
11	34	100.0	34	3 US-09-363-939A-178	Sequence 178, App
12	34	100.0	34	3 US-09-363-939A-179	Sequence 179, App
13	34	100.0	34	3 US-09-363-939A-180	Sequence 180, App
14	34	100.0	34	3 US-09-363-939A-181	Sequence 181, App
15	34	100.0	34	3 US-09-363-939A-182	Sequence 182, App
16	34	100.0	34	3 US-09-363-939A-183	Sequence 183, App
17	34	100.0	34	3 US-09-363-939A-184	Sequence 184, App
18	34	100.0	34	3 US-09-363-939A-185	Sequence 185, App
19	34	100.0	34	3 US-09-363-939A-186	Sequence 186, App
20	34	100.0	34	3 US-09-791-301-174	Sequence 174, App
21	34	100.0	34	3 US-09-791-301-175	Sequence 175, App
22	34	100.0	34	3 US-09-791-301-176	Sequence 176, App
23	34	100.0	34	3 US-09-791-301-177	Sequence 177, App
24	34	100.0	34	3 US-09-791-301-178	Sequence 178, App

ALIGNMENTS

RESULT 1
US-09-363-939A-93
; Sequence 93, Application US/09363939A
; Patient No. 6346611
GENERAL INFORMATION:
; APPLICANT: Pagratis, Nikos
; APPLICANT: Lochrie, Michael
; APPLICANT: Gold, Harry
TITLE OF INVENTION: High Affinity TGFBeta Nucleic Acid Ligands and
FILE REFERENCE: NX87
CURRENT APPLICATION NUMBER: US/09/363, 939A
PRIORITY APPLICATION NUMBER: 09/046, 247
PRIORITY FILING DATE: 1998-03-23
PRIORITY APPLICATION NUMBER: 08/458, 424
PRIORITY FILING DATE: 1995-06-02
PRIORITY APPLICATION NUMBER: 07/714, 131
PRIORITY FILING DATE: 1991-06-10
PRIORITY APPLICATION NUMBER: 07/931, 473
PRIORITY APPLICATION NUMBER: 07/964, 624
PRIORITY FILING DATE: 1992-10-21
PRIORITY APPLICATION NUMBER: 08/117, 991
PRIORITY FILING DATE: 1993-09-08
PRIORITY APPLICATION NUMBER: 07/536, 428
PRIORITY FILING DATE: 1990-06-11
NUMBER OF SEQ ID NOS: 216
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO: 93
SEQ ID NO: 34
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
; NAME/KEY: modified base
; LOCATION: (1)..(34)
; OTHER INFORMATION: All pyrimidines are 2'F.
US-09-363-939A-93
Query Match 100.0%; Score 34; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 5.4e-06;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGAGGUAUUACAGACGUUGUUAUGCGUACUCC 34

Db 1 GGAGGUUUAUACAGAGUCUGUUAUGCUGUACUCC 34

RESULT 2

US-09-363-939A-115

; Sequence 115, Application US/093633939A

; GENERAL INFORMATION:

; APPLICANT: Pagratis, Nikos

; APPLICANT: Lochrie, Michael

; TITLE OF INVENTION: High Affinity TGF β Nucleic Acid Ligands and

; TITLE OF INVENTION: Inhibitors

; FILE REFERENCE: NEX87

; CURRENT APPLICATION NUMBER: US/09/363, 939A

; CURRENT FILING DATE: 1999-07-29

; PRIOR APPLICATION NUMBER: 09/046, 247

; PRIOR FILING DATE: 1998-03-23

; PRIOR APPLICATION NUMBER: 08/458, 424

; PRIOR FILING DATE: 1995-06-02

; PRIOR APPLICATION NUMBER: 07/714, 131

; PRIOR FILING DATE: 1991-06-10

; PRIOR APPLICATION NUMBER: 07/931, 473

; PRIOR FILING DATE: 1992-08-17

; PRIOR APPLICATION NUMBER: 07/964, 624

; PRIOR FILING DATE: 1992-10-21

; PRIOR APPLICATION NUMBER: 08/117, 991

; PRIOR FILING DATE: 1993-09-08

; PRIOR APPLICATION NUMBER: 07/536, 428

; PRIOR FILING DATE: 1990-06-11

; NUMBER OF SEQ ID NOS: 216

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 115

; LENGTH: 34

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: Sequence

; NAME/KEY: modified base

; LOCATION: (1)..(34)

; OTHER INFORMATION: All pyrimidines are 2'F.

US-09-363-939A-115

Query Match 100.0%; Score 34; DB 3; Length 34;

Best Local Similarity 100.0%; Pred. No. 5.4e-06; DB 0;

Matches 0; Indels 0; Gaps 0;

QY 1 GGAGGUUUAUACAGAGUCUGUUAUGCUGUACUCC 34

Do 1 GGAGGUUUAUACAGAGUCUGUUAUGCUGUACUCC 34

RESULT 4

US-09-363-939A-171

; Sequence 171, Application US/093633939A

; Patent No. 634661

; GENERAL INFORMATION:

; APPLICANT: Pagratis, Nikos

; APPLICANT: Gold, Larry, Michael

; TITLE OF INVENTION: High Affinity TGF β Nucleic Acid Ligands and

; FILE REFERENCE: NEX87

; CURRENT APPLICATION NUMBER: US/09/363, 939A

; CURRENT FILING DATE: 1999-07-29

; PRIOR APPLICATION NUMBER: 09/046, 247

; PRIOR FILING DATE: 1998-03-23

; PRIOR APPLICATION NUMBER: 08/458, 424

; PRIOR FILING DATE: 1995-06-02

; PRIOR APPLICATION NUMBER: 07/714, 131

; PRIOR FILING DATE: 1991-06-10

; PRIOR APPLICATION NUMBER: 07/931, 473

; PRIOR FILING DATE: 1992-08-17

; PRIOR APPLICATION NUMBER: 07/964, 624

; PRIOR FILING DATE: 1992-10-21

; PRIOR APPLICATION NUMBER: 08/117, 991

; NUMBER OF SEQ ID NOS: 216

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 171

; LENGTH: 34

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: Sequence

; NAME/KEY: modified base

; LOCATION: (1)..(34)

; OTHER INFORMATION: All pyrimidines are 2'F; a's and g's at positions 1, 5, 8, 11, 13-16, 20, 22, 24-25, 28 and 30 are

; OTHER INFORMATION: 2'-OCH₃; linkage at positions 34 and 35 is 3'-3'.

US-09-363-939A-171

RESULT 3

US-09-363-939A-121

; Sequence 121, Application US/093633939A

; Patent No. 634661

; GENERAL INFORMATION:

; APPLICANT: Pagratis, Nikos

; APPLICANT: Lochrie, Michael

; APPLICANT: Gold, Harry

; TITLE OF INVENTION: Inhibitors

; FILE REFERENCE: NEX87

; CURRENT APPLICATION NUMBER: US/09/363, 939A

; CURRENT FILING DATE: 1999-07-29

; PRIOR APPLICATION NUMBER: 09/046, 247

; PRIOR FILING DATE: 1998-03-23

; PRIOR APPLICATION NUMBER: 08/458, 424

; PRIOR FILING DATE: 1995-06-02

; PRIOR APPLICATION NUMBER: 07/714, 131

; PRIOR FILING DATE: 1991-06-10

; PRIOR APPLICATION NUMBER: 07/931, 473

; PRIOR FILING DATE: 1992-08-17

; PRIOR APPLICATION NUMBER: 07/964, 624

; PRIOR FILING DATE: 1992-10-21

; PRIOR APPLICATION NUMBER: 08/117, 991

; NUMBER OF SEQ ID NOS: 216

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 171

; LENGTH: 34

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: Sequence

; NAME/KEY: modified base

; LOCATION: (1)..(34)

; OTHER INFORMATION: All pyrimidines are 2'F; a's and g's at positions 1, 5, 8, 11, 13-16, 20, 22, 24-25, 28 and 30 are

; OTHER INFORMATION: 2'-OCH₃; linkage at positions 34 and 35 is 3'-3'.

US-09-363-939A-171

Query Match 100.0%; Score 34; DB 3; Length 34;
 Best Local Similarity 100.0%; Pred. No. 5.4e-06; Mismatches 0; Indels 0; Gaps 0;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGGUUAUACAGAGUCUGUAGCUC 34
 Db 1 GGAGGUUAUACAGAGUCUGUAGCUC 34

RESULT 5
 US-09-363-939A-172
 Sequence 172, Application US/09363939A
 Patent No. 6346611
 GENERAL INFORMATION:
 APPLICANT: Pagratis, Nikos
 APPLICANT: Lochrie, Michael
 APPLICANT: Gold, Larry
 TITLE OF INVENTION: High Affinity TGF β Nucleic Acid Ligands and
 TITLE OF INVENTION: Inhibitors
 FILE REFERENCE: NEX87
 CURRENT APPLICATION NUMBER: US/09/363, 939A
 CURRENT FILING DATE: 1999-07-29
 PRIOR APPLICATION NUMBER: 09/046, 247
 PRIOR FILING DATE: 1998-03-23
 PRIOR APPLICATION NUMBER: 08/458, 424
 PRIOR FILING DATE: 1995-06-02
 PRIOR APPLICATION NUMBER: 07/714, 131
 PRIOR FILING DATE: 1991-06-10
 PRIOR APPLICATION NUMBER: 07/931, 473
 PRIOR FILING DATE: 1992-08-17
 PRIOR APPLICATION NUMBER: 07/536, 428
 PRIOR FILING DATE: 1990-06-11
 PRIOR APPLICATION NUMBER: 08/117, 991
 PRIOR FILING DATE: 1993-09-08
 PRIOR APPLICATION NUMBER: 07/536, 428
 PRIOR FILING DATE: 1990-06-11
 NUMBER OF SEQ ID NOS: 216
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 173
 LENGTH: 34
 TYPE: RNA
 ORGANISM: Artificial sequence
 FEATURE: OTHER INFORMATION: Description of Artificial Sequence
 OTHER INFORMATION: Synthetic
 OTHER INFORMATION: Sequence
 NAME/KEY: modified base
 LOCATION: (1)..(34)
 OTHER INFORMATION: All Pyrimidines are 2'F; a's and g's at positions 1-4 are 2'OCN3; linkage at positions 34 and 35 is
 OTHER INFORMATION: 3'-3'.

US-09-363-939A-173
 Query Match 100.0%; Score 34; DB 3; Length 34;
 Best Local Similarity 100.0%; Pred. No. 5.4e-06; Mismatches 0; Indels 0; Gaps 0;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGGUUAUACAGAGUCUGUAGCUC 34
 Db 1 GGAGGUUAUACAGAGUCUGUAGCUC 34

RESULT 6
 US-09-363-939A-173
 Sequence 173, Application US/09363939A
 Patent No. 6346611
 GENERAL INFORMATION:
 APPLICANT: Pagratis, Nikos
 APPLICANT: Lochrie, Michael
 APPLICANT: Gold, Larry
 TITLE OF INVENTION: High Affinity TGF β Nucleic Acid Ligands and
 TITLE OF INVENTION: Inhibitors
 FILE REFERENCE: NEX87
 CURRENT APPLICATION NUMBER: US/09/363, 939A
 CURRENT FILING DATE: 1999-07-29
 PRIOR APPLICATION NUMBER: 09/046, 247
 PRIOR FILING DATE: 1998-03-23
 PRIOR APPLICATION NUMBER: 08/458, 424
 PRIOR FILING DATE: 1995-06-02
 PRIOR APPLICATION NUMBER: 07/714, 131
 PRIOR FILING DATE: 1991-06-10
 PRIOR APPLICATION NUMBER: 07/931, 473
 PRIOR FILING DATE: 1992-08-17
 PRIOR APPLICATION NUMBER: 07/536, 428
 PRIOR FILING DATE: 1990-06-11
 NUMBER OF SEQ ID NOS: 216
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 174
 LENGTH: 34
 TYPE: RNA
 ORGANISM: Artificial sequence

FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Sequence
 NAME/KEY: modified base
 LOCATION: (1)..(34)
 OTHER INFORMATION: All pyrimidines are 2'F; a's and g's at positions 5, 8, and 11 are 2'-OCH₃; linkage at positions 34 and 35 is 3'-3'.

Query Match 100.0%; Score 34; DB 3; Length 34;
 Best Local Similarity 100.0%; Pred. No. 5.4e-06; Mismatches 0; Indels 0; Gaps 0;
 Matches 34; Conservative 0; MisMatches 0; Indels 0; Gaps 0;
 Qy 1 GCGAGGUAUUACAGAGUCUGUAVAGCUGUACCC 34
 Db 1 GGAGGUAUUACAGAGUCUGUAVAGCUGUACCC 34

RESULT 8
 US-09-363-939A-175
 Sequence 175, Application US/09363939A
 Patent No. 6346611
 GENERAL INFORMATION:
 GENERAL INFORMATION:
 APPLICANT: Pigratis, Nikos
 APPLICANT: Gold, Harry
 APPLICANT: Lochrie, Michael
 APPLICANT: Gold, Larry
 TITLE OF INVENTION: High Affinity TGF β Nucleic Acid Ligands and
 FILE REFERENCE: Inhibitors
 CURRENT APPLICATION NUMBER: US/09/363, 939A.
 CURRENT FILING DATE: 1999-07-29
 PRIOR APPLICATION NUMBER: 09/046, 247
 PRIOR FILING DATE: 1998-03-23
 PRIOR APPLICATION NUMBER: 08/458, 424
 PRIOR FILING DATE: 1995-06-02
 PRIOR APPLICATION NUMBER: 07/714, 131
 PRIOR FILING DATE: 1991-06-10
 PRIOR APPLICATION NUMBER: 07/931, 473
 PRIOR FILING DATE: 1992-08-17
 PRIOR APPLICATION NUMBER: 07/964, 624
 PRIOR FILING DATE: 1990-06-11
 PRIOR APPLICATION NUMBER: 07/536, 428
 PRIOR FILING DATE: 1991-06-10
 PRIOR APPLICATION NUMBER: 09/046, 247
 PRIOR FILING DATE: 1998-03-23
 PRIOR APPLICATION NUMBER: 08/458, 424
 PRIOR FILING DATE: 1995-06-02
 PRIOR APPLICATION NUMBER: 07/714, 131
 PRIOR FILING DATE: 1991-06-10
 PRIOR APPLICATION NUMBER: 07/931, 473
 PRIOR FILING DATE: 1992-08-17
 PRIOR APPLICATION NUMBER: 07/964, 624
 PRIOR FILING DATE: 1990-06-11
 NUMBER OF SEQ ID NOS: 216
 SEQ ID NO: 1-76
 LENGTH: 34
 TYPE: RNA
 ORGANISM: Artificial Sequence
 FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Sequence
 NAME/KEY: modified base
 LOCATION: (1)..(34)
 OTHER INFORMATION: All pyrimidines are 2'F; a's and g's at positions 5, 8, and 11 are 2'-OCH₃; linkage at positions 34 and 35 is 3'-3'.

Query Match 100.0%; Score 34; DB 3; Length 34;
 Best Local Similarity 100.0%; Pred. No. 5.4e-06; Mismatches 0; Indels 0; Gaps 0;
 Matches 34; Conservative 0; MisMatches 0; Indels 0; Gaps 0;
 Qy 1 GAGGGUAUUACAGAGUCUGUAVAGCUGUACCC 34
 Db 1 GGAGGUAUUACAGAGUCUGUAVAGCUGUACCC 34

RESULT 9
 US-09-363-939A-176
 Query Match 100.0%; Score 34; DB 3; Length 34;
 Best Local Similarity 100.0%; Pred. No. 5.4e-06; Mismatches 0; Indels 0; Gaps 0;
 Matches 34; Conservative 0; MisMatches 0; Indels 0; Gaps 0;
 Qy 1 GGAGGUAUUACAGAGUCUGUAVAGCUGUACCC 34
 Db 1 GGAGGUAUUACAGAGUCUGUAVAGCUGUACCC 34

RESULT 9
 US-09-363-939A-176

PRIOR APPLICATION NUMBER: 08/458,424
 PRIOR FILING DATE: 1995-06-02
 PRIOR APPLICATION NUMBER: 07/714,131
 PRIOR FILING DATE: 1991-06-10
 PRIOR APPLICATION NUMBER: 07/931,473
 PRIOR FILING DATE: 1992-08-17
 PRIOR APPLICATION NUMBER: 07/964,624
 PRIOR FILING DATE: 1992-10-21
 PRIOR APPLICATION NUMBER: 08/117,991
 PRIOR FILING DATE: 1993-09-08
 PRIOR APPLICATION NUMBER: 07/536,428
 PRIOR FILING DATE: 1990-06-11
 NUMBER OF SEQ ID NOS: 216
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 180
 LENGTH: 34
 TYPE: RNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Sequence
 NAME/KEY: modified base
 LOCATION: (1)..(34)
 OTHER INFORMATION: All pyrimidines are 2'F; a's and g's at positions 1-5, 8, 11, 25 and 30 are 2'-OCH₃; linkage at positions 34 and 35 is 3'-3'.
 US-09-363-939A-180

Query Match 100 0%; Score 34; DB 3; Length 34;
 Best Local Similarity 100.0%; Pred. No. 5.4e-06;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QV 1 GGAGGUUAAUCAGAGUCGUUAAGCUGUACUCC 34
 DB 1 GGAGGUUAAUCAGAGUCGUUAAGCUGUACUCC 34

RESULT 15
 US-09-363-939A-182
 ; Sequence 182, Application US/09363939A
 ; Patent No. 6346611
 ; GENERAL INFORMATION:
 ; APPLICANT: Pagratis, Nikos
 ; APPLICANT: Lochrie, Michael
 ; TITLE OF INVENTION: High Affinity TGF β Nucleic Acid Ligands and FILE REFERENCE: NEX87
 ; CURRENT APPLICATION NUMBER: US/09/363,939A
 ; CURRENT FILING DATE: 1999-07-29
 ; PRIOR APPLICATION NUMBER: 09/046,247
 ; PRIOR FILING DATE: 1995-06-02
 ; PRIOR APPLICATION NUMBER: 08/458,424
 ; PRIOR FILING DATE: 1998-03-23
 ; PRIOR APPLICATION NUMBER: 07/931,473
 ; PRIOR FILING DATE: 1990-06-11
 ; PRIOR APPLICATION NUMBER: 07/964,624
 ; PRIOR FILING DATE: 1992-10-21
 ; PRIOR APPLICATION NUMBER: 08/117,991
 ; PRIOR FILING DATE: 1993-09-08
 ; PRIOR APPLICATION NUMBER: 07/536,428
 ; PRIOR FILING DATE: 1990-06-11
 ; NUMBER OF SEQ ID NOS: 216
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 182
 LENGTH: 34
 TYPE: RNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Sequence
 NAME/KEY: modified base
 LOCATION: (1)..(34)
 OTHER INFORMATION: All pyrimidines are 2'F; a's and g's at positions 1-5, 8, 11, 13-16, 24-25, 28 and 30 are 2'-OCH₃; linkage at positions 34 and 35 is 3'-3'.
 US-09-363-939A-182

Query Match 100 0%; Score 34; DB 3; Length 34;
 Best Local Similarity 100.0%; Pred. No. 5.4e-06;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QV 1 GGAGGUUAAUCAGAGUCGUUAAGCUGUACUCC 34
 DB 1 GGAGGUUAAUCAGAGUCGUUAAGCUGUACUCC 34

Search completed: December 27, 2005, 16:45:24
 Job time : 146 secs

OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Sequence
 NAME/KEY: modified_base

GenCore version 5.1.6
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Om nucleic - nucleic search, using sw model
Run on: December 27, 2005, 14:58:35 ; Search time 815 Seconds
344.980 Million cell updates/sec

Title: US-10-812-642-115
Perfect score: 34

Sequence: 1 ggagguaauacagacuauagcguauacucc 34

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqb, 413469005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA_Main:
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2: /cgn2_6/ptodata/1/pubpna/us08_pubcomb.seq: *
3: /cgn2_6/ptodata/1/pubpna/us09_pubcomb.seq: *
4: /cgn2_6/ptodata/1/pubpna/us09a_pubcomb.seq: *
5: /cgn2_6/ptodata/1/pubpna/us10_pubcomb.seq: *
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10: /cgn2_6/ptodata/1/pubpna/us11_pubcomb.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

24	34	100.0	34	8	US-10-762-915-6	Sequence 6, Appli
25	34	100.0	34	8	US-10-762-915-7	Sequence 7, Appli
26	34	100.0	34	8	US-10-762-915-8	Sequence 8, Appli
27	34	100.0	34	8	US-10-762-915-21	Sequence 21, Appli
28	34	100.0	34	8	US-10-762-915-22	Sequence 22, Appli
29	34	100.0	34	8	US-10-762-915-27	Sequence 27, Appli
30	34	100.0	34	8	US-10-762-915-148	Sequence 148, App
31	34	100.0	34	8	US-10-812-642-93	Sequence 93, Appli
32	34	100.0	34	8	US-10-812-642-115	Sequence 115, App
33	34	100.0	34	8	US-10-812-642-121	Sequence 121, App
34	34	100.0	34	8	US-10-812-642-171	Sequence 171, App
35	34	100.0	34	8	US-10-812-642-172	Sequence 172, App
36	34	100.0	34	8	US-10-812-642-173	Sequence 173, App
37	34	100.0	34	8	US-10-812-642-174	Sequence 174, App
38	34	100.0	34	8	US-10-812-642-175	Sequence 175, App
39	34	100.0	34	8	US-10-812-642-176	Sequence 176, App
40	34	100.0	34	8	US-10-812-642-177	Sequence 177, App
41	34	100.0	34	8	US-10-812-642-178	Sequence 178, App
42	34	100.0	34	8	US-10-812-642-179	Sequence 179, App
43	34	100.0	34	8	US-10-812-642-180	Sequence 180, App
44	34	100.0	34	8	US-10-812-642-181	Sequence 181, App
45	34	100.0	34	8	US-10-812-642-182	Sequence 182, App

Query Match Similarity 100.0%; Score 34; DB 3; Length 34;
Matches 34; Conservative 100.0%; Mismatches 0; Indels 0; Gaps 0;

RESULT 1
US-09-791-301-93
; Sequence 93, Application US/09791301
Publication No. US20030064943A1
GENERAL INFORMATION:
APPLICANT: Pagratis, Nikos
APPLICANT: Lochrie, Michael
TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and
TITLE OF INVENTION: Inhibitors
FILE REFERENCE: NEX 87/C
CURRENT APPLICATION NUMBER: US/09-791,301
CURRENT FILING DATE: 2001-02-23
PRIORITY APPLICATION NUMBER: 09/046,247
PRIORITY FILING DATE: 1998-01-23
PRIORITY APPLICATION NUMBER: 08/458,424
PRIORITY FILING DATE: 1995-06-02
PRIORITY APPLICATION NUMBER: 07/714,131
PRIORITY FILING DATE: 1991-06-10
PRIORITY APPLICATION NUMBER: 07/931,473
PRIORITY FILING DATE: 1992-08-17
PRIORITY APPLICATION NUMBER: 07/964,624
PRIORITY FILING DATE: 1992-10-21
PRIORITY APPLICATION NUMBER: 08/117,991
PRIORITY FILING DATE: 1993-09-08
PRIORITY APPLICATION NUMBER: 07/536,428
PRIORITY FILING DATE: 1990-06-11
PRIORITY APPLICATION NUMBER: 09/363,939
PRIORITY FILING DATE: 1999-07-29
NUMBER OF SEQ ID NOS: 216
SOFTWARE: PatentIn Ver. 2.0
SEQUENCE ID NO 93
LENGTH: 34
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
SEQUENCE: US-09-791-301-178
SEQUENCE: US-09-791-301-179
SEQUENCE: US-09-791-301-180
SEQUENCE: US-09-791-301-181
SEQUENCE: US-09-791-301-182
SEQUENCE: US-09-791-301-183
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SEQUENCE: US-09-791-301-185
SEQUENCE: US-09-791-301-186
SEQUENCE: US-10-718-833-12
SEQUENCE: US-10-762-915-1
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SEQUENCE: US-10-762-915-361
SEQUENCE: US-10

QY 1 GGAGGUUAUACAGAGUCGUUAUGCGUACUCC 34
 ; Sequence 115, Application US/09791301
 ; Publication No. US20030064943A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pagratis, Nikos
 ; APPLICANT: Lochrie, Michael
 ; APPLICANT: Gold, Larry
 ; TITLE OF INVENTION: High Affinity TGF β Nucleic Acid Ligands and
 ; FILE REFERENCE: NEX 87/C
 ; CURRENT APPLICATION NUMBER: US/09/791, 301
 ; CURRENT FILING DATE: 2001-02-23
 ; PRIOR APPLICATION NUMBER: 09/046, 247
 ; PRIOR FILING DATE: 1998-03-23
 ; PRIOR APPLICATION NUMBER: 08/458, 424
 ; PRIOR FILING DATE: 1995-06-02
 ; PRIOR APPLICATION NUMBER: 07/714, 131
 ; PRIOR FILING DATE: 1991-06-10
 ; PRIOR APPLICATION NUMBER: 07/931, 473
 ; PRIOR FILING DATE: 1992-08-17
 ; PRIOR APPLICATION NUMBER: 07/964, 624
 ; PRIOR FILING DATE: 1990-06-11
 ; PRIOR APPLICATION NUMBER: 09/363, 939
 ; PRIOR FILING DATE: 1999-07-29
 ; NUMBER OF SEQ ID NOS: 216
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 115
 ; LENGTH: 34
 ; TYPE: RNA
 ; FEATURE: Artificial Sequence
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; NAME/KEY: modified base
 ; LOCATION: (1)..(34)
 ; OTHER INFORMATION: All pyrimidines are 2'-F.
 ; US-09-791-301-115
 ; SEQ ID NO 115
 ; LENGTH: 34
 ; TYPE: RNA
 ; FEATURE: Artificial Sequence
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; NAME/KEY: modified base
 ; LOCATION: (1)..(34)
 ; OTHER INFORMATION: All pyrimidines are 2'-F.
 ; US-09-791-301-115
 ; Query Match 100.0%; Score 34; DB 3; Length 34;
 ; Best Local Similarity 100.0%; Pred. No. 2.8e-05;
 ; Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ; GENERAL INFORMATION:
 ; APPLICANT: Pagratis, Nikos
 ; APPLICANT: Lochrie, Michael
 ; APPLICANT: Gold, Larry
 ; TITLE OF INVENTION: High Affinity TGF β Nucleic Acid Ligands and
 ; FILE REFERENCE: NEX 87/C
 ; CURRENT APPLICATION NUMBER: US/09/791, 301
 ; PRIOR APPLICATION NUMBER: 09/046, 247
 ; PRIOR FILING DATE: 1998-03-23
 ; PRIOR APPLICATION NUMBER: 08/458, 424
 ; PRIOR FILING DATE: 1995-06-02
 ; PRIOR APPLICATION NUMBER: 07/714, 131
 ; PRIOR FILING DATE: 1991-06-10
 ; PRIOR APPLICATION NUMBER: 07/931, 473
 ; PRIOR FILING DATE: 1992-08-17
 ; PRIOR APPLICATION NUMBER: 07/964, 624
 ; PRIOR FILING DATE: 1999-07-29
 ; NUMBER OF SEQ ID NOS: 216
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 171
 ; LENGTH: 34
 ; TYPE: RNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Sequence
 NAME/KEY: modified base
 LOCATION: (1)..(34)
 OTHER INFORMATION: All Pyrimidines are 2'F; a's and 9's at positions 8, 11, 13-16, 20, 22, 24-25, 28 and 30 are 2'-OCH₃; linkage at positions 34 and 35 is 3'-3'.

US-09-791-301-171

Query Match 100.0%; Score 34; DB 3; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.8e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GGAGGUUUAUACAGAGUCUGUAUAGCUCACCC 34
 Db 1 GGAGGUUUAUACAGAGUCUGUAUAGCUCACCC 34

RESULT 5

US-09-791-301-172

Sequence 172, Application US/09791301
 Publication No. US20030064943A1
 GENERAL INFORMATION:
 APPLICANT: Pagratis, Nikos
 APPLICANT: Gold, Larry
 APPLICANT: Lochrie, Michael
 APPLICANT: Gold, Larry
 TITLE OF INVENTION: High Affinity TGF β Nucleic Acid Ligands and
 FILE REFERENCE: NEX 87/C
 CURRENT APPLICATION NUMBER: US/09/791,301
 PRIOR APPLICATION NUMBER: 09/046,247
 PRIOR FILING DATE: 1998-03-23
 PRIOR APPLICATION NUMBER: 08/458,424
 PRIOR FILING DATE: 1995-06-02
 PRIOR APPLICATION NUMBER: 07/714,131
 PRIOR FILING DATE: 1991-06-10
 PRIOR APPLICATION NUMBER: 09/046,247
 PRIOR FILING DATE: 1998-03-23
 PRIOR APPLICATION NUMBER: 08/458,424
 PRIOR FILING DATE: 1995-06-02
 PRIOR APPLICATION NUMBER: 07/714,131
 PRIOR FILING DATE: 1991-06-10
 PRIOR APPLICATION NUMBER: 07/931,473
 PRIOR FILING DATE: 1992-08-17
 PRIOR APPLICATION NUMBER: 07/964,624
 PRIOR FILING DATE: 1992-10-21
 PRIOR APPLICATION NUMBER: 08/117,991
 PRIOR FILING DATE: 1993-09-08
 PRIOR APPLICATION NUMBER: 07/536,428
 PRIOR FILING DATE: 1990-06-11
 PRIOR APPLICATION NUMBER: 09/363,939
 PRIOR FILING DATE: 1999-07-29
 NUMBER OF SEQ ID NOS: 216
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 173
 LENGTH: 34

TYPE: RNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Sequence
 NAME/KEY: modified base
 LOCATION: (1)..(34)
 OTHER INFORMATION: All Pyrimidines are 2'F; a's and 9's at positions 8, 11, 13-16, 20, 22, 24-25, 28 and 30 are 2'-OCH₃; linkage at positions 34 and 35 is 3'-3'.

US-09-791-301-173
 Query Match 100.0%; Score 34; DB 3; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.8e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GGAGGUUUAUACAGAGUCUGUAUAGCUCACCC 34
 Db 1 GGAGGUUUAUACAGAGUCUGUAUAGCUCACCC 34

RESULT 6

OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Sequence
 NAME/KEY: modified base
 LOCATION: (1)..(34)
 OTHER INFORMATION: All Pyrimidines are 2'F; a's and 9's at positions 8, 11, 13-16, 20, 22, 24-25, 28 and 30 are 2'-OCH₃; linkage at positions 34 and 35 is 3'-3'.

US-09-791-301-174
 Query Match 100.0%; Score 34; DB 3; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.8e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GGAGGUUUAUACAGAGUCUGUAUAGCUCACCC 34
 Db 1 GGAGGUUUAUACAGAGUCUGUAUAGCUCACCC 34

Query Match 100.0%; Score 34; DB 3; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.8e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GGAGGUUUAUACAGAGUCUGUAUAGCUCACCC 34
 Db 1 GGAGGUUUAUACAGAGUCUGUAUAGCUCACCC 34

RESULT 6

PRIOR APPLICATION NUMBER: 07/954, 624
 PRIOR FILING DATE: 1992-10-21
 PRIOR APPLICATION NUMBER: 08/117, 991
 PRIOR FILING DATE: 1993-09-08
 PRIOR APPLICATION NUMBER: 07/536, 428
 PRIOR FILING DATE: 1990-06-11
 PRIOR APPLICATION NUMBER: 09/363, 939
 PRIOR FILING DATE: 1999-07-29
 NUMBER OF SEQ ID NOS: 216
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 174
 LENGTH: 34
 TYPE: RNA
 ORGANISM: Artificial Sequence
 FEATURE: OTHER INFORMATION: Description of Artificial sequence: Synthetic
 OTHER INFORMATION: Sequence
 NAME/KEY: modified base
 LOCATION: (1)..(34)
 OTHER INFORMATION: All pyrimidines are 2'F; a's and g's at positions 13-16 are 2'-OCH3; linkage at positions 34 and 35
 OTHER INFORMATION: 13-16 are 2'-OCH3; linkage at positions 34 and 35
 OTHER INFORMATION: 18 3'-3'.
 US-09-791-301-174
 Query Match 100.0%; Score 34; DB 3; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2,8e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGAGGUTUATACAGAGUCUGUAGCUGUACCC 34
 Db 1 GGAGGUTUATACAGAGUCUGUAGCUGUACCC 34
 RESULT 8
 US-09-791-301-175
 Sequence 175 Application US/09791301
 Publication No. US20030064943A1
 GENERAL INFORMATION:
 APPLICANT: Pagratis, Nikos
 APPLICANT: Lochrie, Michael
 APPLICANT: Gold, Larry
 APPLICANT: Gold, Larry
 TITLE OF INVENTION: High Affinity TGF β Nucleic Acid Ligands and
 TITLE OF INVENTION: Inhibitors
 TITLE REFERENCE: NEX 87/C
 CURRENT APPLICATION NUMBER: US/09/791, 301
 CURRENT FILING DATE: 2001-02-23
 PRIOR APPLICATION NUMBER: 09/046, 247
 PRIOR APPLICATION NUMBER: 09/046, 247
 PRIOR FILING DATE: 1998-03-23
 PRIOR APPLICATION NUMBER: 08/458, 424
 PRIOR FILING DATE: 1995-06-02
 PRIOR APPLICATION NUMBER: 07/714, 131
 PRIOR FILING DATE: 1991-06-10
 PRIOR APPLICATION NUMBER: 07/931, 473
 PRIOR FILING DATE: 1992-08-17
 PRIOR APPLICATION NUMBER: 08/458, 424
 PRIOR FILING DATE: 1995-06-02
 PRIOR APPLICATION NUMBER: 07/714, 131
 PRIOR FILING DATE: 1991-06-10
 PRIOR APPLICATION NUMBER: 07/931, 473
 PRIOR FILING DATE: 1992-08-17
 PRIOR APPLICATION NUMBER: 07/964, 624
 PRIOR FILING DATE: 1992-10-21
 PRIOR APPLICATION NUMBER: 08/117, 991
 PRIOR FILING DATE: 1993-09-08
 PRIOR APPLICATION NUMBER: 07/536, 428
 PRIOR FILING DATE: 1990-06-11
 PRIOR APPLICATION NUMBER: 09/363, 939
 PRIOR FILING DATE: 1999-07-29
 NUMBER OF SEQ ID NOS: 216
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 176
 LENGTH: 34
 TYPE: RNA
 ORGANISM: Artificial Sequence
 FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Sequence
 NAME/KEY: modified base
 LOCATION: (1)..(34)
 OTHER INFORMATION: All pyrimidines are 2'F; a's and g's at positions 13-16 are 2'-OCH3; linkage at positions 34 and 35
 OTHER INFORMATION: 13-16 are 2'-OCH3; linkage at positions 34 and 35
 OTHER INFORMATION: 18 3'-3'.
 US-09-791-301-176
 Query Match 100.0%; Score 34; DB 3; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2,8e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGAGGUTUATACAGAGUCUGUACCC 34
 Db 1 GGAGGUTUATACAGAGUCUGUACCC 34
 RESULT 9
 US-09-791-301-176
 Sequence 176 Application US/09791301
 Publication No. US20030064943A1
 GENERAL INFORMATION:
 APPLICANT: Pagratis, Nikos
 APPLICANT: Lochrie, Michael
 APPLICANT: Gold, Larry
 APPLICANT: Gold, Larry
 TITLE OF INVENTION: High Affinity TGF β Nucleic Acid Ligands and
 TITLE OF INVENTION: Inhibitors
 FILE REFERENCE: NEX 87/C
 CURRENT APPLICATION NUMBER: US/09/791, 301
 CURRENT FILING DATE: 2001-02-23
 PRIOR APPLICATION NUMBER: 09/046, 247
 PRIOR FILING DATE: 1998-03-23
 PRIOR APPLICATION NUMBER: 08/458, 424
 PRIOR FILING DATE: 1995-06-02
 PRIOR APPLICATION NUMBER: 07/714, 131
 PRIOR FILING DATE: 1991-06-10
 PRIOR APPLICATION NUMBER: 07/931, 473
 PRIOR FILING DATE: 1992-08-17
 PRIOR APPLICATION NUMBER: 08/458, 424
 PRIOR FILING DATE: 1995-06-02
 PRIOR APPLICATION NUMBER: 07/714, 131
 PRIOR FILING DATE: 1991-06-10
 PRIOR APPLICATION NUMBER: 07/931, 473
 PRIOR FILING DATE: 1992-08-17
 PRIOR APPLICATION NUMBER: 07/964, 624
 PRIOR FILING DATE: 1992-10-21
 PRIOR APPLICATION NUMBER: 08/117, 991
 PRIOR FILING DATE: 1993-09-08
 PRIOR APPLICATION NUMBER: 07/536, 428
 PRIOR FILING DATE: 1990-06-11
 PRIOR APPLICATION NUMBER: 09/363, 939
 PRIOR FILING DATE: 1999-07-29
 NUMBER OF SEQ ID NOS: 216
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 176
 LENGTH: 34
 TYPE: RNA
 ORGANISM: Artificial Sequence
 FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Sequence
 NAME/KEY: modified base
 LOCATION: (1)..(34)
 OTHER INFORMATION: All pyrimidines are 2'F; a's and g's at positions 13-16 are 2'-OCH3; linkage at positions 34 and 35
 OTHER INFORMATION: 13-16 are 2'-OCH3; linkage at positions 34 and 35
 OTHER INFORMATION: 18 3'-3'.
 US-09-791-301-176
 Query Match 100.0%; Score 34; DB 3; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2,8e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGAGGUTUATACAGAGUCUGUACCC 34
 Db 1 GGAGGUTUATACAGAGUCUGUACCC 34
 RESULT 10
 US-09-791-301-177
 Sequence 177 Application US/09791301
 Publication No. US20030064943A1
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Sequence
 NAME/KEY: modified base

GENERAL INFORMATION:
 APPLICANT: Pigratis, Nikos
 APPLICANT: Lochrie, Michael
 APPLICANT: Gold, Larry
 TITLE OF INVENTION: High Affinity TGF β Nucleic Acid Ligands and
 FILE REFERENCE: NEX 87/C
 CURRENT APPLICATION NUMBER: US/09/791,301
 CURRENT FILING DATE: 2001-02-23
 PRIOR APPLICATION NUMBER: 09/046,247
 PRIOR FILING DATE: 1998-03-23
 PRIOR APPLICATION NUMBER: 08/458,424
 PRIOR FILING DATE: 1995-06-02
 PRIOR APPLICATION NUMBER: 07/714,131
 PRIOR FILING DATE: 1991-06-10
 PRIOR APPLICATION NUMBER: 07/931,473
 PRIOR FILING DATE: 1992-08-17
 PRIOR APPLICATION NUMBER: 07/964,624
 PRIOR FILING DATE: 1992-10-21
 PRIOR APPLICATION NUMBER: 08/117,991
 PRIOR FILING DATE: 1993-09-08
 PRIOR APPLICATION NUMBER: 07/536,428
 PRIOR FILING DATE: 1990-06-11
 PRIOR APPLICATION NUMBER: 09/363,939
 PRIOR FILING DATE: 1999-07-29
 NUMBER OF SEQ ID NOS: 216
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 178
 LENGTH: 34
 TYPE: RNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Sequence
 NAME/KEY: modified base
 LOCATION: (1)..(34)
 OTHER INFORMATION: All pyrimidines are 2'-F; g at position 20 is
 US-09-791-301-178
 OTHER INFORMATION: 2'-OCH₃; linkage at positions 34 and 35 is 3'-3'.
 Query Match 100.0%; Score 34; DB 3; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.8e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 34; Conservative 0; Other Information: and 35 is 3'-3'.
 Query 1 |||GAGGUUACAGAGUCGUUAAGCUC 34
 Db 1 GGAGGUUACAGAGUCGUUAAGCUC 34
 LENGTH: 34
 TYPE: RNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Sequence
 NAME/KEY: modified base
 LOCATION: (1)..(34)
 OTHER INFORMATION: All pyrimidines are 2'-F; g at position 20 is
 US-09-791-301-179
 OTHER INFORMATION: 2'-OCH₃; linkage at positions 34 and 35 is 3'-3'.
 Query Match 100.0%; Score 34; DB 3; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.8e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 34; Conservative 0; Other Information: and 35 is 3'-3'.
 RESULT 11
 US-09-791-301-179
 Sequence 178, Application US/09791301
 Publication No. US20030064943A1
 GENERAL INFORMATION:
 APPLICANT: Pigratis, Nikos
 APPLICANT: Lochrie, Michael
 APPLICANT: Gold, Larry
 TITLE OF INVENTION: Inhibitors
 FILE REFERENCE: NEX 87/C
 CURRENT APPLICATION NUMBER: US/09/791,301
 PRIOR APPLICATION NUMBER: 09/046,247
 PRIOR FILING DATE: 1998-03-23
 PRIOR APPLICATION NUMBER: 08/458,424
 PRIOR FILING DATE: 1995-06-02
 PRIOR APPLICATION NUMBER: 07/714,131
 PRIOR FILING DATE: 1991-06-10
 PRIOR APPLICATION NUMBER: 07/931,473
 PRIOR FILING DATE: 1992-10-21
 PRIOR APPLICATION NUMBER: 08/117,991
 PRIOR FILING DATE: 1993-09-08
 PRIOR APPLICATION NUMBER: 07/536,428
 PRIOR FILING DATE: 1990-06-11
 PRIOR APPLICATION NUMBER: 09/363,939
 PRIOR FILING DATE: 1999-07-29
 NUMBER OF SEQ ID NOS: 216
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 179
 LENGTH: 34
 TYPE: RNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Sequence
 NAME/KEY: modified base
 LOCATION: (1)..(34)
 OTHER INFORMATION: All pyrimidines are 2'-F; a at position 22 is 3'-3'.
 OTHER INFORMATION: 2'-OCH₃; linkage at positions 34 and 35 is 3'-3'.
 US-09-791-301-179

Query Match
Best Local Similarity 100.0%; Pred. No. 2.8e-05; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGAGGUUUAUACAGAGUCUGUAGCUGUACUCC 34

Db 1 GGAGGUUUAUACAGAGUCUGUAGCUGUACUCC 34

RESULT 13
US-09-791-301-180
Sequence 180, Application US/09791301
Publication No. US20030064943A1
GENERAL INFORMATION:
APPLICANT: Pagratis, Nikos
APPLICANT: Lochrie, Michael
APPLICANT: Gold, Larry
TITLE OF INVENTION: High Affinity TGF β Nucleic Acid Ligands and
Title of Invention: Inhibitors
CURRENT APPLICATION NUMBER: US/09/791,301
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 09/046,247
PRIOR FILING DATE: 1998-03-23
PRIOR APPLICATION NUMBER: 08/458,424
PRIOR APPLICATION NUMBER: 08/458,424
PRIOR FILING DATE: 1995-06-02
PRIOR APPLICATION NUMBER: 07/714,131
PRIOR FILING DATE: 1992-08-17
PRIOR APPLICATION NUMBER: 07/931,473
PRIOR FILING DATE: 1992-08-17
PRIOR APPLICATION NUMBER: 07/954,624
PRIOR FILING DATE: 1992-10-21
PRIOR APPLICATION NUMBER: 08/117,991
PRIOR FILING DATE: 1993-07-29
PRIOR APPLICATION NUMBER: 08/117,991
PRIOR FILING DATE: 1993-09-08
PRIOR APPLICATION NUMBER: 07/536,428
PRIOR FILING DATE: 1990-06-11
PRIOR APPLICATION NUMBER: 09/363,939
PRIOR FILING DATE: 1999-07-29
NUMBER OF SEQ ID NOS: 216
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO: 181
LENGTH: 34
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
NAME/KEY: modified base
LOCATION: (1)..(34)
OTHER INFORMATION: All Pyrimidines are 2'F; a's and g's at positions 1, 5, 8, 11, 25 and 30 are 2'-OCH₃; linkage at positions 3, 4 and 35 is 3'-3'.

US-09-791-301-180
Query Match
Best Local Similarity 100.0%; Score 34; DB 3; Length 34;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGAGGUUUAUACAGAGUCUGUAGCUGUACUCC 34

Db 1 GGAGGUUUAUACAGAGUCUGUAGCUGUACUCC 34

RESULT 14
US-09-791-301-181
Sequence 181, Application US/09791301
Publication No. US20030064943A1
GENERAL INFORMATION:
APPLICANT: Pagratis, Nikos
APPLICANT: Lochrie, Michael
APPLICANT: Gold, Larry
TITLE OF INVENTION: High Affinity TGF β Nucleic Acid Ligands and
Title of Invention: Inhibitors
FILE REFERENCE: NEX 87/C
CURRENT APPLICATION NUMBER: US/09/791,301
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 09/046,247
PRIOR FILING DATE: 1998-03-23
PRIOR APPLICATION NUMBER: 08/458,424
PRIOR FILING DATE: 1995-06-02
PRIOR APPLICATION NUMBER: 07/714,131
PRIOR FILING DATE: 1992-08-17
PRIOR APPLICATION NUMBER: 07/931,473
PRIOR FILING DATE: 1992-08-17
PRIOR APPLICATION NUMBER: 07/954,624
PRIOR FILING DATE: 1995-10-21
PRIOR APPLICATION NUMBER: 08/117,991
PRIOR FILING DATE: 1993-09-08
PRIOR APPLICATION NUMBER: 07/536,428
PRIOR FILING DATE: 1990-06-11
PRIOR APPLICATION NUMBER: 09/363,939
PRIOR FILING DATE: 1999-07-29
NUMBER OF SEQ ID NOS: 216
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO: 181
LENGTH: 34
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
NAME/KEY: modified base
LOCATION: (1)..(34)
OTHER INFORMATION: All Pyrimidines are 2'F; a's and g's at positions 1, 5, 8, 11, 25 and 30 are 2'-OCH₃; linkage at positions 3, 4 and 35 is 3'-3'.

US-09-791-301-182
Sequence 182, Application US/09791301
Publication No. US20030064943A1
GENERAL INFORMATION:
APPLICANT: Pagratis, Nikos
APPLICANT: Lochrie, Michael
APPLICANT: Gold, Larry
TITLE OF INVENTION: High Affinity TGF β Nucleic Acid Ligands and
Title of Invention: Inhibitors
FILE REFERENCE: NEX 87/C
CURRENT APPLICATION NUMBER: US/09/791,301
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 09/046,247
PRIOR FILING DATE: 1998-03-23
PRIOR APPLICATION NUMBER: 07/931,473
PRIOR FILING DATE: 1992-08-17
PRIOR APPLICATION NUMBER: 07/954,624
PRIOR FILING DATE: 1995-06-02
PRIOR APPLICATION NUMBER: 07/714,131
PRIOR FILING DATE: 1991-06-10
PRIOR APPLICATION NUMBER: 07/931,473
PRIOR FILING DATE: 1992-08-17
PRIOR APPLICATION NUMBER: 07/954,624
PRIOR FILING DATE: 1992-10-21
PRIOR APPLICATION NUMBER: 08/117,991
PRIOR FILING DATE: 1993-09-08
PRIOR APPLICATION NUMBER: 07/536,428
PRIOR FILING DATE: 1990-06-11
PRIOR APPLICATION NUMBER: 09/363,939
PRIOR FILING DATE: 1999-07-29

NUMBER OF SEQ ID NOS: 216
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 182
LENGTH: 34
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Sequence
NAME/KEY: modified base
LOCATION: (11)..(34)
OTHER INFORMATION: All pyrimidines are 2'F: a's and g's at positions 15, 8, 11, 13-16, 24-25, 28 and 30 are 2'-OCH3;
OTHER INFORMATION: linkage at positions 34 and 35 is 3'-3'.
OTHER INFORMATION: linkge at positions 34 and 35 is 3'-3'.
US-09-791-301-182

Query Match 100.0%; Score 34; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.8e-05; Length 34;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Caps 0;
Oy 1 GAGGUUUAUCAGAGUCGUAGCUC 34
Db 1 GAGGUUUAUCAGAGUCGUAGCUC 34

Search completed: December 27, 2005, 16:59:16
Job time : 816 sec

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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 27, 2005, 15:06:46 ; Search time 296 Seconds
(without alignments)
59.610 Million cell updates/sec

Title: US-10-812-642-115
Perfect score: 34
Sequence: 1 ggggguaauuacagagucuguaugcugucucc 34

Scoring table: IDENTITY_NUC
Gappp 10.0 , Gapext 1.0

Searched: 4169288 seqB, 259477437 residues

Total number of hits satisfying chosen parameters: 8336576

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match: 0*
Maximum Match: 100*
Listing first 45 summaries

Database :

1: /cgn2_6/podata/2/pubpna/US08_NEW_PUB.seq: *
2: /cgn2_6/podata/2/pubpna/US05_NEW_PUB.seq: *
3: /cgn2_6/podata/2/pubpna/US07_NEW_PUB.seq: *
4: /cgn2_6/podata/2/pubpna/PCT_NEW_PUB.seq: *
5: /cgn2_6/podata/2/pubpna/US05_NEW_PUB.seq: *
6: /cgn2_6/podata/2/pubpna/US10_NEW_PUB.seq: *
7: /cgn2_6/podata/2/pubpna/US11_NEW_PUB.seq: *
8: /cgn2_6/podata/2/pubpna/US11_NEW_PUB.seq2: *
9: /cgn2_6/podata/2/pubpna/US60_NEW_PUB.seq: *
10: /cgn2_6/podata/2/pubpna/US60_NEW_PUB.seq: *

Result No. , Score

Result No.	Score	Query Match Length	DB ID	Description
1	20.2	59.4	150481	7 US-11-112-908-37 Sequence 37, Appl
2	20.2	59.4	171162	7 US-11-112-908-38 Sequence 38, Appl
3	19.2	56.5	691	6 US-10-950-185-64880 Sequence 64880, A
4	19.2	56.5	2279	6 US-10-950-185-57144 Sequence 57144, A
5	18.6	54.7	971	6 US-10-950-185-62416 Sequence 62416, A
6	18.6	54.7	1527	6 US-10-950-185-3371 Sequence 3371, A
7	18.4	54.1	1086	6 US-10-950-185-51403 Sequence 51403, A
8	18.2	53.5	25	7 US-11-121-849-617034 Sequence 167034, A
9	18.2	53.5	435	6 US-10-950-185-51403 Sequence 51403, A
10	18.2	53.5	435	6 US-10-950-185-51403 Sequence 51403, A
11	18.2	53.5	1671	6 US-10-950-185-56074 Sequence 56074, A
12	18.2	53.5	1094	6 US-10-950-561-248 Sequence 248, Appl
13	18.2	53.5	2439	6 US-10-950-561-248 Sequence 248, Appl
14	18.2	53.5	2789	6 US-10-995-561-250 Sequence 250, Appl
15	18.2	53.5	20991	6 US-10-995-561-13488 Sequence 13488, A
16	18.2	53.5	31657	6 US-10-995-561-13334 Sequence 13334, A
17	18.2	53.5	33175	6 US-10-995-561-13270 Sequence 13270, A
18	18	52.9	5134	7 US-11-960-005-1 Sequence 1, Appl
19	18	52.9	6160	7 US-11-960-005-1 Sequence 3, Appl
20	18	52.9	148220	7 US-11-121-086-90 Sequence 90, Appl
21	18	52.9	207600	7 US-11-112-908-31 Sequence 31, Appl
22	17.8	52.4	201	6 US-10-995-561-53173 Sequence 53173, Appl
23	17.8	52.4	201	6 US-10-995-561-74017 Sequence 74017, A

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

Sequence 109, APP
Sequence 1197, APP
Sequence 13567, APP
Sequence 1352, APP
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Sequence 16421, APP
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Sequence 3892, APP
Sequence 4443, APP
Sequence 4092, APP
Sequence 24, APP
Sequence 81, APP

CURRENT FILING DATE: 2005-04-22
 PRIORITY APPLICATION NUMBER: US 60/564,758
 PRIORITY FILING DATE: 2004-04-23
 PRIORITY APPLICATION NUMBER: US 60/575,978
 PRIORITY FILING DATE: 2004-06-01
 PRIORITY APPLICATION NUMBER: US 60/631,702
 PRIORITY FILING DATE: 2004-11-30
 PRIORITY APPLICATION NUMBER: US 60/633,826
 PRIORITY FILING DATE: 2004-12-07
 NUMBER OF SEQ ID NOS: 511
 SOFTWARE: PatentIN version 3.3
 SEQ ID NO 38
 LENGTH: 171162
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-11-112-908-38

Query Match
 Best Local Similarity 59.4%; Score 20.2; DB 7; Length 171162;
 Matches 16; Conservative 9; Mismatches 8; Indels 0; Gaps 0;
 Qy 1 GAGGGGUUACAGAGCAGUAGCAGGUACUC 33
 Db 139691 GTAGATTTACAGAGCTTATAGCATTAGTC 139659

RESULT 3
 US-10-750-185-64880
 Sequence 64880, Application US/10750185
 Publication No. US20050260603A1
 GENERAL INFORMATION:
 APPLICANT: MMI GENOMICS, INC.
 APPLICANT: DENISE, Sue K.
 APPLICANT: KERR, Richard
 APPLICANT: ROSENFIELD, David
 APPLICANT: HOLM, Tom
 APPLICANT: BATES, Stephen
 APPLICANT: FANTIN, Dennis
 TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
 FILE REFERENCE: NM11100-2
 CURRENT APPLICATION NUMBER: US/10/750,185
 CURRENT FILING DATE: 2003-12-31
 PRIORITY APPLICATION NUMBER: US 60/437,482
 PRIORITY FILING DATE: 2002-12-31
 NUMBER OF SEQ ID NOS: 64922
 SOFTWARE: PatentIN version 3.1
 SEQ ID NO 64880
 LENGTH: 691
 TYPE: DNA
 ORGANISM: Bovine 198668800808150
 US-10-750-185-64880

Query Match
 Best Local Similarity 56.5%; Score 19.2; DB 6; Length 691;
 Matches 12; Conservative 9; Mismatches 3; Indels 0; Gaps 0;
 Qy 6 UAUAUACAGAGCAGUAGCUGU 29
 Db 450 TCAATTACAGGGCTGTAGTTG 473

RESULT 4
 US-10-750-185-57144-C
 Sequence 57144, Application US/10750185
 Publication No. US20050260603A1
 GENERAL INFORMATION:
 APPLICANT: MMI GENOMICS, INC.
 APPLICANT: DENISE, Sue K.
 APPLICANT: KERR, Richard
 APPLICANT: ROSENFIELD, David
 APPLICANT: HOLM, Tom
 APPLICANT: BATES, Stephen
 APPLICANT: FANTIN, Dennis
 APPLICANT: FANTIN, Dennis

RESULT 5
 US-10-750-185-62416/C
 Sequence 62416, Application US/10750185
 Publication No. US20050260603A1
 GENERAL INFORMATION:
 APPLICANT: MMI GENOMICS, INC.
 APPLICANT: DENISE, Sue K.
 APPLICANT: KERR, Richard
 APPLICANT: ROSENFIELD, David
 APPLICANT: HOLM, Tom
 APPLICANT: BATES, Stephen
 APPLICANT: FANTIN, Dennis
 TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
 FILE REFERENCE: NM11100-2
 CURRENT APPLICATION NUMBER: US/10/750,185
 CURRENT FILING DATE: 2003-12-31
 PRIORITY APPLICATION NUMBER: US 60/437,482
 PRIORITY FILING DATE: 2002-12-31
 NUMBER OF SEQ ID NOS: 64922
 SOFTWARE: PatentIN version 3.1
 SEQ ID NO 62416
 LENGTH: 971
 TYPE: DNA
 ORGANISM: Bovine 198668800400331
 US-10-750-185-62416

Query Match
 Best Local Similarity 54.7%; Score 18.6; DB 6; Length 971;
 Matches 14; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
 Qy 10 UACAGAGCAGUAGCUGUCC 34
 Db 173 TACAGACTGAGTTAGCTGTAGTAC 149

RESULT 6
 US-10-750-185-33471
 Sequence 33471, Application US/10750185
 Publication No. US20050260603A1
 GENERAL INFORMATION:
 APPLICANT: MMI GENOMICS, INC.
 APPLICANT: DENISE, Sue K.
 APPLICANT: KERR, Richard
 APPLICANT: ROSENFIELD, David
 APPLICANT: HOLM, Tom
 APPLICANT: BATES, Stephen
 APPLICANT: FANTIN, Dennis
 TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
 FILE REFERENCE: NM11100-2
 CURRENT APPLICATION NUMBER: US/10/750,185

CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 6,922
; SOFTWARE: PATENTIN version 3.1
; SEQ ID NO: 33471
; LENGTH: 1527
; TYPE: DNA
; ORGANISM: Bovine 198668802040664
; US-10-750-185-33471

Query Match 54.7%; Score 18.6; DB 6; Length 1527;
Best Local Similarity 45.5%; Pred. No. 29; Mismatches 9; Indels 0; Gaps 0;
Matches 15; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

RESULT 7
US-10-750-185-51403/C
; Sequence 51403, Application US/10750185
; Publication No. US0050606031
; GENERAL INFORMATION:
; APPLICANT: MMi GENOMICS, INC.
; APPLICANT: DENISE, SUE K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFIELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 6,922
; SOFTWARE: PATENTIN version 3.1
; SEQ ID NO 51403
; LENGTH: 1086
; TYPE: DNA
; ORGANISM: Bovine 19866880936749
; US-10-750-185-51403

Query Match 54.1%; Score 18.4; DB 6; Length 1086;
Best Local Similarity 57.1%; Pred. No. 33; Mismatches 6; Indels 0; Gaps 0;
Matches 16; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
; SEQ ID NO 1042
; LENGTH: 1015

RESULT 8
US-11-121-849-617034/C
; Sequence 617034, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3664.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Microarray Probe Sequence Listing Generator v 1.1
; SEQ ID NO 617034
; LENGTH: 25
; TYPE: DNA

Query Match 53.5%; Score 18.2; DB 7; Length 435;
Best Local Similarity 48.4%; Pred. No. 34; Mismatches 8; Indels 0; Gaps 0;
Matches 15; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

RESULT 9
US-10-467-657-263
; Sequence 263, Application US/10467657
; Publication No. US0050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA, Maria Rita
; APPLICANT: PIZZA, Mariagrazia
; APPLICANT: MONACI, Elisabetta
; APPLICANT: MASIGNANI, Vega
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 263
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
; US-10-467-657-263

Query Match 53.5%; Score 18.2; DB 6; Length 435;
Best Local Similarity 48.4%; Pred. No. 34; Mismatches 8; Indels 0; Gaps 0;
Matches 15; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

RESULT 10
US-10-467-657-3599
; Sequence 3599, Application US/10467657
; Publication No. US0050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA, Maria Rita
; APPLICANT: PIZZA, Mariagrazia
; APPLICANT: MASIGNANI, Vega
; APPLICANT: MONACI, Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3599
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
; US-10-467-657-3599

Query Match 53.5%; Score 18.2; DB 6; Length 435;
Best Local Similarity 48.4%; Pred. No. 34; Mismatches 8; Indels 0; Gaps 0;

Qy 4 GGTGAAUACAGAGUCUGUAGCUGUAC 34
; Sequence 56074, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFIELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: FANTIN, Deans
; APPLICANT: BATES, Stephen
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIORITY APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentsIN version 3.1
; SEQ ID NO 5674
; LENGTH: 1671
; TYPE: DNA
; ORGANISM: Bovine 19866881576202

RESULT 11
US-10-750-185-56074

Query Match 53.5%; Score 18.2; DB 6; Length 1671;
Best Local Similarity 60.9%; Pred. No. 44; Mismatches 3; Indels 0; Gaps 0;
Matches 14; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Oy 1 GGAGGUUAUACAGAGUCUGUAU 23
Db 365 GGAGGTATTACAGATCTGAT 343

Qy 4 GGTGAAUACAGAGUCUGUAC 34
; Sequence 56074, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 250
; LENGTH: 2789
; TYPE: DNA
; ORGANISM: Homo sapiens

RESULT 12
US-10-995-561-248

Query Match 53.5%; Score 18.2; DB 6; Length 1671;
Best Local Similarity 58.1%; Pred. No. 49; Mismatches 5; Indels 0; Gaps 0;
Matches 18; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Oy 4 GGTGAAUACAGAGUCUGUAC 34
Db 365 GGAGGTATTACAGATCTGAT 343

Qy 4 GGTGAAUACAGAGUCUGUAC 34
; Sequence 56074, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 248
; LENGTH: 1894
; TYPE: DNA
; ORGANISM: Homo sapiens

RESULT 13
US-10-995-561-248

Query Match 53.5%; Score 18.2; DB 6; Length 1894;
Best Local Similarity 58.1%; Pred. No. 45; Mismatches 8; Indels 0; Gaps 0;
Matches 18; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Oy 1 GGAGGUUAUACAGAGUCUGUAU 31
Db 169 GGAGGTATTACAGACCTGAAA 199

RESULT 14
US-10-995-561-250

Query Match 53.5%; Score 18.2; DB 6; Length 2439;
Best Local Similarity 58.1%; Pred. No. 48; Mismatches 8; Indels 0; Gaps 0;
Matches 18; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Oy 1 GGAGGUUAUACAGAGUCUGUAU 31
Db 974 GGTGGTCATACAGACCTGAAA 1004

Qy 4 GGTGAAUACAGAGUCUGUAC 34
; Sequence 56074, Application US/10750185
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 250
; LENGTH: 2789
; TYPE: DNA
; ORGANISM: Homo sapiens

RESULT 15
US-10-995-561-1348B/C

Query Match 53.5%; Score 18.2; DB 6; Length 2789;
Best Local Similarity 58.1%; Pred. No. 49; Mismatches 8; Indels 0; Gaps 0;
Matches 18; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Oy 1 GGAGGUUAUACAGAGUCUGUAU 31
Db 974 GGTGGTCATACAGACCTGAAA 1004

Qy 4 GGTGAAUACAGAGUCUGUAC 34
; Sequence 1348B, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1348B
; LENGTH: 20991
; TYPE: DNA
; ORGANISM: Homo sapiens

RESULT 16
US-10-995-561-1348B

Qy 4 GGTGAAUACAGAGUCUGUAC 34
; Sequence 1348B, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1348B
; LENGTH: 20991
; TYPE: DNA
; ORGANISM: Homo sapiens

RESULT 17
US-10-995-561-1348B

Qy 4 GGTGAAUACAGAGUCUGUAC 34
; Sequence 1348B, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1348B
; LENGTH: 20991
; TYPE: DNA
; ORGANISM: Homo sapiens

RESULT 18
US-10-995-561-1348B

Qy 4 GGTGAAUACAGAGUCUGUAC 34
; Sequence 1348B, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1348B
; LENGTH: 20991
; TYPE: DNA
; ORGANISM: Homo sapiens

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On nucleic - nucleic search, using sw model

Run on:

December 27, 2005, 13:28:20 ; Search time 1988 Seconds

(without alignments) 972.172 Million cell updates/sec

Title: US-10-812-642-115

Perfect score:

Sequence: 1 ggagguauuacagagucuagucuacucc 34

Scoring table:

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Gapext 1.0

Searched:

5883141 seqB, 28421725653 residues

Total number of hits satisfying chosen parameters:

11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBml:

*

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gb_bp:*

2:

gb_in:*

3:

gb_env:*

4:

gb_om:*

5:

gb_ov:*

6:

gb_ptt:*

7:

gb_ph:*

8:

gb_pr:*

9:

gb_rn:*

10:

gb_st:*

11:

gb_ex:*

12:

gb_un:*

13:

gb_xr:*

14:

gb_hg:*

15:

gb_pf:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	34	100.0	34	6 AR193289 AR193289 Sequence
2	34	100.0	34	6 AR193311 AR193311 Sequence
3	34	100.0	34	6 AR193317 AR193317 Sequence
4	34	100.0	34	6 AR193361 AR193361 Sequence
5	34	100.0	34	6 AR193362 AR193362 Sequence
6	34	100.0	34	6 AR193363 AR193363 Sequence
7	34	100.0	34	6 AR193364 AR193364 Sequence
8	34	100.0	34	6 AR193365 AR193365 Sequence
9	34	100.0	34	6 AR193366 AR193366 Sequence
10	34	100.0	34	6 AR193367 AR193367 Sequence
11	34	100.0	34	6 AR193368 AR193368 Sequence
12	34	100.0	34	6 AR193369 AR193369 Sequence
13	34	100.0	34	6 AR193370 AR193370 Sequence
14	34	100.0	34	6 AR193371 AR193371 Sequence
15	34	100.0	34	6 AR193372 AR193372 Sequence
16	34	100.0	34	6 AR193373 AR193373 Sequence
17	34	100.0	34	6 AR193374 AR193374 Sequence
18	34	100.0	34	6 AR193375 AR193375 Sequence

ALIGNMENTS									
RESULT 1									
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LOCUS									
DEFINITION									
ACCESSION									
VERSION									
KEYWORDS									
SOURCE									
ORGANISM									
REFERENCE									
AUTHORS									
TITLE									
JOURNAL									
FEATURES									
source									
1. (bases 1 to 34)									
REFERENCE									
Pagratis,N., Lochrie,M. and Gold,L.									
High affinity TGF beta, nucleic acid ligands and inhibitors									
TITLE									
Patent: US 6346611-A 93-12-FEB-2002;									
JOURNAL									
FEATURES									
source									
1. .34									
/organism="unknown"									
/mol_type="unassigned" DNA"									
ORIGIN									
Query									
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Length									
DB									
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Best									
Local									
Similarity									
23;									
Conservative									
11;									
Mismatches									
0;									
Indels									
0;									
Gaps									
0;									
RESULT 2									
AR193311									
LOCUS									
DEFINITION									
ACCESSION									
VERSION									
KEYWORDS									
SOURCE									
ORGANISM									
Unclassified.									
REFERENCE									
1 (bases 1 to 34)									
AUTHORS									
Pagratis,N., Lochrie,M. and Gold,L.									

AR193376 Sequence				
AR491289 Sequence				
AR491311 Sequence				
AR491317 Sequence				
AR491367 Sequence				
AR491362 Sequence				
AR491363 Sequence				
AR491364 Sequence				
AR491365 Sequence				
AR491366 Sequence				
AR491367 Sequence				
AR491368 Sequence				
AR491369 Sequence				
AR491370 Sequence				
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AR491372 Sequence				
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AR193311 Sequence				
AR491288 Sequence				
AR491312 Sequence				
AR491313 Sequence				
AR4913287 Sequence				

FEATURES	Patent: US 6346611-A 174 12-FEB-2002; Location/Qualifiers
Source	1. .34 /organism="unassigned" /mol_type="unassigned DNA"
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Qy	Query Match 100.0%; Score 34; DB 6; Length 34; Best Local Similarity 67.6%; Pred. No. 0. 0.0024; 0; Indels 0; Gaps 0;
Db	1 GGAGGTTTACAGAGCTGTAGCTGACTCC 34
RESULT 8	
AR193365	
LOCUS	AR193365 34 bp DNA
DEFINITION	Sequence 175 from patent US 6346611.
ACCESSION	AR193365
VERSION	AR193365.1 GI:20239330
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1. (bases 1 to 34)
AUTHORS	Pagratis,N., Lochrie,M. and Gold,L.
TITLE	High affinity TGF-beta, nucleic acid ligands and inhibitors
JOURNAL	Patent: US 6346611-A 175 12-FEB-2002; Location/Qualifiers
FEATURES	1. .34 /organism="unassigned DNA"
ORIGIN	
Qy	Query Match 100.0%; Score 34; DB 6; Length 34; Best Local Similarity 67.6%; Pred. No. 0.0024; 0; Mismatches 0; Indels 0; Gaps 0;
Db	1 GGAGGTTTACAGAGCTGTAGCTGACTCC 34
RESULT 9	
AR193366	
DEFINITION	Sequence 176 from patent US 6346611.
ACCESSION	AR193366
VERSION	AR193366.1 GI:20239331
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1. (bases 1 to 34)
AUTHORS	Pagratis,N., Lochrie,M. and Gold,L.
TITLE	High affinity TGF-beta, nucleic acid ligands and inhibitors
JOURNAL	Patent: US 6346611-A 176 12-FEB-2002; Location/Qualifiers
FEATURES	1. .34 /organism="unassigned DNA"
ORIGIN	
Qy	Query Match 100.0%; Score 34; DB 6; Length 34; Best Local Similarity 67.6%; Pred. No. 0. 0.0024; 0; Indels 0; Gaps 0;
Db	1 GGAGGTTTACAGAGCTGTAGCTGACTCC 34
RESULT 10	
AR193367	
LOCUS	AR193367 34 bp DNA
DEFINITION	Sequence 177 from patent US 6346611.
ACCESSION	AR193367
VERSION	AR193367.1 GI:20239332
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1. (bases 1 to 34)
AUTHORS	Pagratis,N., Lochrie,M. and Gold,L.
TITLE	High affinity TGF-beta, nucleic acid ligands and inhibitors
JOURNAL	Patent: US 6346611-A 177 12-FEB-2002; Location/Qualifiers
FEATURES	1. .34 /organism="unassigned DNA"
ORIGIN	
Qy	Query Match 100.0%; Score 34; DB 6; Length 34; Best Local Similarity 67.6%; Pred. No. 0. 0.0024; 0; Indels 0; Gaps 0;
Db	1 GGAGGTTTACAGAGCTGTAGCTGACTCC 34
RESULT 11	
AR193368	
LOCUS	AR193368 34 bp DNA
DEFINITION	Sequence 178 from patent US 6346611.
ACCESSION	AR193368
VERSION	AR193368.1 GI:20239333
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1. (bases 1 to 34)
AUTHORS	Pagratis,N., Lochrie,M. and Gold,L.
TITLE	High affinity TGF-beta, nucleic acid ligands and inhibitors
JOURNAL	Patent: US 6346611-A 178 12-FEB-2002; Location/Qualifiers
FEATURES	1. .34 /organism="unassigned DNA"
ORIGIN	
Qy	Query Match 100.0%; Score 34; DB 6; Length 34; Best Local Similarity 67.6%; Pred. No. 0. 0.0024; 0; Indels 0; Gaps 0;
Db	1 GGAGGTTTACAGAGCTGTAGCTGACTCC 34
RESULT 12	
AR193369	
LOCUS	AR193369 34 bp DNA
DEFINITION	Sequence 179 from patent US 6346611.
ACCESSION	AR193369
VERSION	AR193369.1 GI:20239334
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1. (bases 1 to 34)
AUTHORS	Pagratis,N., Lochrie,M. and Gold,L.
TITLE	High affinity TGF-beta, nucleic acid ligands and inhibitors
JOURNAL	Patent: US 6346611-A 179 12-FEB-2002;
FEATURES	
ORIGIN	
Qy	Query Match 100.0%; Score 34; DB 6; Length 34; Best Local Similarity 67.6%; Pred. No. 0. 0.0024; 0; Mismatches 0; Indels 0; Gaps 0;
Db	1 GGAGGTTTACAGAGCTGTAGCTGACTCC 34

FEATURES
Source

Query Match
Best Local Similarity 67.6%; Pred. No. 0.00024; Length 34;
Matches 23; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

ORIGIN

Query Match
Best Local Similarity 67.6%; Pred. No. 0.00024; Length 34;
Matches 23; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

Oy
Db

1 GAGGGTATTACAGAGTCGTAGCTGACTCC 34

RESULT 13

AR193370

DEFINITION Sequence 180 from patent US 6346611.

ACCESSION AR193370

VERSION AR193370.1

KEYWORDS .

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 34)

AUTHORS Pagratis,N., Lochee,M. and Gold,L.

TITLE High affinity TGF beta, nucleic acid ligands and inhibitors

JOURNAL Patent: US 6346611-A 180 12-FEB-2002;

FEATURES

Source

1. .34
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/mol_type="unassigned DNA"

ORIGIN

Query Match
Best Local Similarity 67.6%; Pred. No. 0.00024; Length 34;
Matches 23; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

Oy
Db

1 GAGGGTATTACAGAGTCGTAGCTGACTCC 34

RESULT 14

AR193371

DEFINITION Sequence 181 from patent US 6346611.

ACCESSION AR193371

VERSION AR193371.1

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 34)

AUTHORS Pagratis,N., Lochee,M. and Gold,L.

TITLE High affinity TGF beta, nucleic acid ligands and inhibitors

JOURNAL Patent: US 6346611-A 181 12-FEB-2002;

FEATURES

Source

1. .34
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match
Best Local Similarity 67.6%; Pred. No. 0.00024; Length 34;
Matches 23; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

ORIGIN

Query Match
Best Local Similarity 67.6%; Pred. No. 0.00024; Length 34;
Matches 23; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

RESULT 15

AR193372

DEFINITION Sequence 182 from patent US 6346611.

ACCESSION AR193372

VERSION AR193372.1

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 34)

AUTHORS Pagratis,N., Lochee,M. and Gold,L.

TITLE High affinity TGF beta, nucleic acid ligands and inhibitors

JOURNAL Patent: US 6346611-A 182 12-FEB-2002;

FEATURES

Source

1. .34
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match
Best Local Similarity 67.6%; Pred. No. 0.00024; Length 34;
Matches 23; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

ORIGIN

Query Match
Best Local Similarity 67.6%; Pred. No. 0.00024; Length 34;
Matches 23; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: December 27, 2005, 12:44:50 ; Search time 487 Seconds
(without alignments)
465.297 Million cell updates/sec

Title: US-10-812-642-115
Perfect score: 34
Sequence: 1 ggagguauuacagacuguaugcugacucc 34

Scoring table: IDENTITY_NUC
Gapov 10.0 , Gapext 1.0
Searched: 4996597 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: geneseqn1900s;*
2: geneseqn1950s;*
3: geneseqn2000s;*
4: geneseqn2001s;*
5: geneseqn2001bs;*
6: geneseqn2002as;*
7: geneseqn2002bs;*
8: geneseqn2003as;*
9: geneseqn2003bs;*
10: geneseqn2003s;*
11: geneseqn2003ds;*
12: geneseqn2004as;*
13: geneseqn2004bs;*
14: geneseqn2005s;*

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	34	100.0	34 5 AAF90818	AAF90818 TGFbeta2
2	34	100.0	34 5 AAF90873	AAF90873 NX22284 1
3	34	100.0	34 5 AAF90877	AAF90877 NX22284 1
4	34	100.0	34 5 AAF90796	AAF90796 TGFbeta2
5	34	100.0	34 5 AAF90870	AAF90870 NX22284 1
6	34	100.0	34 5 AAF90883	AAF90883 NX22284 1
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8	34	100.0	34 5 AAF90869	AAF90869 NX22284 1
9	34	100.0	34 5 AAF90875	AAF90875 NX22284 1
10	34	100.0	34 5 AAF90872	AAF90872 NX22284 1
11	34	100.0	34 5 AAF90879	AAF90879 NX22284 1
12	34	100.0	34 5 AAF90882	AAF90882 NX22284 1
13	34	100.0	34 5 AAF90868	AAF90868 NX22284 1
14	34	100.0	34 5 AAF90876	AAF90876 NX22284 1
15	34	100.0	34 5 AAF90871	AAF90871 NX22284 1
16	34	100.0	34 5 AAF90881	AAF90881 NX22284 1
17	34	100.0	34 5 AAF90878	AAF90878 NX22284 1
18	34	100.0	34 5 AAF90874	AAF90874 NX22284 1
19	34	100.0	34 5 AAF90880	AAF90880 NX22284 1

20 34 100.0 34 12 ADO9385 TGFbeta-Add59385 TGFbeta-Add59391 Monodentate
21 34 100.0 34 12 ADO9391 Monodentate
22 34 100.0 34 13 ADQ89377 Human TGF
23 34 100.0 34 13 ADQ89381 Human TGF
24 34 100.0 34 13 ADQ89390 Human TGF
25 34 100.0 34 13 ADQ89376 Human TGF
26 34 100.0 34 13 ADQ89383 Human TGF
27 34 100.0 34 13 ADQ89377 Human TGF
28 34 100.0 34 13 ADQ89382 Human TGF
29 34 100.0 34 13 ADQ893510 Human TGF
30 34 100.0 34 13 ADQ89520 Human TGF
31 34 100.0 34 13 AEA28125 Human TGF
32 34 100.0 36 5 AAF90795 Human TGF
33 34 100.0 36 5 AAF90817 Human TGF
34 34 100.0 37 5 AAF90819 Human TGF
35 34 100.0 43 5 AAF90794 Human TGF
36 34 100.0 56 5 AAF90793 Human TGF
37 34 100.0 57 5 AAF90792 Human TGF
38 34 100.0 65 13 ADQ89454 Human TGF
39 34 100.0 70 5 AAF90790 Human TGF
40 34 100.0 82 13 ADQ89398 Human TGF
41 33 97.1 33 5 AAF90802 Human TGF
42 33 97.1 33 5 AAF90821 Human TGF
43 33 97.1 65 5 AAF90864 Human TGF
44 32 95.3 70 5 AAF90791 Human TGF
45 32 94.1 32 5 AAF90822 Human TGF

ALIGNMENTS

RESULT 1
ID AAF90818 standard; RNA; 34 BP.
XX AAF90818;
XX
DT 03-MAY-2001 (first entry)
DB TGFbeta2 ligand 21a-21 truncate #28.
XX Human; transforming growth factor beta2; TGFbeta2; SELEX; KW systemic evolution of ligands by exponential enrichment; BS.
XX OS Homo sapiens.
XX
PN WO200109156-A1.
XX
PD 08-FEB-2001.
XX
PP 26-JUL-2000; 2000WO-US020397.
XX
PR 29-JUL-1999; 99US-00363939.
XX
PA (NEXUS-) NEWSTAR PHARM INC.
XX
PT Pagratis N, Lochrie M, Gold L;
XX
DR WPI; 2001-218217/22.
XX
PT New RNA ligand to human transforming growth factor beta2 (TGFbeta2). The
XX pharmaceuticals, diagnostics and as immunohistochemical reagents.
XX
PS Claim 1; Page 70, 178pp; English.
XX
CC The present invention relates to non-naturally occurring, high-affinity
CC RNA ligands to human transforming growth factor beta2 (TGFbeta2). The
CC oligonucleotide ligands were identified by the SELEX method (SELEX stands
CC for Systemic Evolution of Ligands by EXponential Enrichment). The
CC oligonucleotide ligands are useful in any process in which binding to
CC TGFbeta2 is required. The ligands may be useful as pharmaceuticals,
CC diagnostics, imaging agents and immunohistochemical reagents. The present
CC sequence is an oligonucleotide used in the present invention.

XX	WPI; 2001-218217/22.
XX	New RNA ligand to human transforming growth factor beta2, useful as pharmaceuticals, diagnostics and as immunohistochemical reagents.
XX	Claim 1; Page 68; 178pp; English.
XX	The present invention relates to non-naturally occurring, high-affinity RNA ligands to human transforming growth factor beta2 (TGFbeta2). The oligonucleotide ligands were identified by the SELEX method (SELEX stands for Systemic Evolution of Ligands by Exponential Enrichment). The oligonucleotide ligands are useful in any process in which binding to TGFbeta2 is required. The ligands may be useful as pharmaceuticals, diagnostics, imaging agents and immunohistochemical reagents. The present sequence is an oligonucleotide used in the present invention.
XX	Sequence 34 BP; 8 A; 6 C; 9 G; 0 T; 11 U; 0 Other;
XX	Query Match 100.0%; Score 34; DB 5; Length 34;
XX	Best Local Similarity 100.0%; Pred. No. 4.8e-05;
XX	Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	1 GGAGGUUUAUACAGAGUCGUUAUCAGUCGUUC 34
DB	1 GGAGGUUUAUACAGAGUCGUUAUCAGUCGUUC 34
RESULT 5	
ID	AAF90870 standard; RNA; 34 BP.
XX	
AC	AAF90870;
XX	
DT	03-MAY-2001 (first entry)
XX	
DE	NX22284 ligand variant #3.
XX	
KW	Human; transforming growth factor beta2; TGFbeta2; SELEX;
KW	systemic evolution of ligands by exponential enrichment; ss.
OS	Homo sapiens.
XX	
PN	WO200109156-A1.
XX	
PD	08-FEB-2001.
XX	
PF	26-JUL-2000; 20000W0-US020397.
XX	
PR	29-JUL-1999; 99US-00363939.
XX	
PA	(NEXSTAR PHARM INC.
XX	
PI	Pagratis N, Lochrie M, Gold L;
XX	
DR	WPI; 2001-218217/22.
XX	
PT	New RNA ligand to human transforming growth factor beta2, useful as pharmaceuticals, diagnostics and as immunohistochemical reagents.
XX	Claim 1; Page 78; 178pp; English.
XX	The present invention relates to non-naturally occurring, high-affinity RNA ligands to human transforming growth factor beta2 (TGFbeta2). The oligonucleotide ligands were identified by the SELEX method (SELEX stands for Systemic Evolution of Ligands by Exponential Enrichment). The oligonucleotide ligands are useful in any process in which binding to TGFbeta2 is required. The ligands may be useful as pharmaceuticals, diagnostics, imaging agents and immunohistochemical reagents. The present sequence is an oligonucleotide used in the present invention.
XX	Sequence 34 BP; 8 A; 6 C; 9 G; 0 T; 11 U; 0 Other;
XX	
CC	
PS	
SQ	

Qy 1 GGAGGUUAUACAGAGUCUGUUAAGCUGUACUCC 34
 XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1 GGAGGUUAUACAGAGUCUGUUAAGCUGUACUCC 34

RESULT 10
 AAF9072
 ID AAF9072 standard; RNA; 34 BP.
 XX
 AC AAF9072;
 XX DT 03-MAY-2001 (first entry)
 DE NX22284 ligand variant #5.
 KW Human; transforming growth factor beta2; TGFbeta2; SELEX; systemic evolution of ligands by exponential enrichment; ss.
 KW Homo sapiens.
 OS XX
 XX PS WO200109156-A1.
 XX PD 08-FEB-2001.
 XX PF 26-JUL-2000; 2000WO-US020397.
 XX PR 29-JUL-1999; 99US-00363939.
 XX PA (NEXS-) NEXSTAR PHARM INC.
 XX PI Pagratis N, Lochrie M, Gold L;
 DR XX
 DR WPI; 2001-218217/22.

XX New RNA ligand to human transforming growth factor beta2, useful as pharmaceuticals, diagnostics and as immunohistochemical reagents.
 XX PT pharmaceuticals, diagnostics and as immunohistochemical reagents.
 XX PS Claim 1; Page 78; 178pp; English.

CC The present invention relates to non-naturally occurring, high-affinity RNA ligands to human transforming growth factor beta2 (TGFbeta2). The CC oligonucleotide ligands were identified by the SELEX method (SELEX stands for Systemic Evolution of Ligands by Exponential Enrichment). The CC oligonucleotide ligands are useful in any process in which binding to CC TGFbeta2 is required. The ligands may be useful as pharmaceuticals, CC diagnostics, imaging agents and immunohistochemical reagents. The present CC sequence is an oligonucleotide used in the present invention

XX Sequence 34 BP; 8 A; 6 C; 9 G; 0 T; 11 U; 0 Other;

SQ Query Macch 100.0%; Score 34; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 4.8e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGGUUAUACAGAGUCUGUUAAGCUGUACUCC 34
 Db 1 GGAGGUUAUACAGAGUCUGUUAAGCUGUACUCC 34

RESULT 12
 AAF9082
 ID AAF9082 standard; RNA; 34 BP.
 XX
 AC AAF9082;
 XX DT 03-MAY-2001 (first entry)
 XX DE NX22284 ligand variant #15.
 XX KW Human; transforming growth factor beta2; TGFbeta2; SELEX; systemic evolution of ligands by exponential enrichment; ss.
 OS Homo sapiens.
 OS XX PS WO200109156-A1.
 XX PD 08-FEB-2001.
 XX PF 26-JUL-2000; 2000WO-US020397.
 XX PR 29-JUL-1999; 99US-00363939.
 XX PA (NEXS-) NEXSTAR PHARM INC.
 XX PI Pagratis N, Lochrie M, Gold L;
 DR XX
 DR WPI; 2001-218217/22.

XX New RNA ligand to human transforming growth factor beta2, useful as pharmaceuticals, diagnostics and as immunohistochemical reagents.

PS Claim 1; Page 78; 178pp; English.

XX

CC The present invention relates to non-naturally occurring, high-affinity RNA ligands to human transforming growth factor beta2 (TGFbeta2). The CC oligonucleotide ligands were identified by the SELEX method (SELEX stands for Systemic Evolution of Ligands by Exponential Enrichment). The CC oligonucleotide ligands are useful in any process in which binding to CC TGFbeta2 is required. The ligands may be useful as pharmaceuticals, diagnostics, imaging agents and immunohistochemical reagents. The present CC sequence is an oligonucleotide used in the present invention.

XX

SQ Sequence 34 BP; 8 A; 6 C; 9 G; 0 T; 11 U; 0 Other;

Query Match 100.0%; Score 34; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.8e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGGUUUAUACAGAGUCUGUAGCUCUCC 34

Db 1 GGAGGUUUAUACAGAGUCUGUAGCUCUCC 34

RESULT 13

ID AAF90868 standard; RNA; 34 BP.

XX AAF90868;

XX 03-MAY-2001 (first entry)

XX NX22284 ligand variant #1.

DE Human; transforming growth factor beta2; TGFbeta2; SELEX; Systemic evolution of ligands by exponential enrichment; BB.

XX

XX Human; transforming growth factor beta2; TGFbeta2; SELEX; Systemic evolution of ligands by exponential enrichment; BB.

XX Homo sapiens.

XX WO200109156-A1.

XX 08-FEB-2001.

XX 26-JUL-2000; 2000WO-US020397.

XX PR 29-JUL-1999; 99US-00363939.

XX PA (NEXS-) NEXSTAR PHARM INC.

XX PI Pagratis N, Lochrie M, Gold L;

XX DR WPI; 2001-218217/22.

XX PT New RNA ligand to human transforming growth factor beta2, useful as pharmaceuticals, diagnostics and as immunohistochemical reagents.

XX

PS Claim 1; Page 78; 178pp; English.

XX The present invention relates to non-naturally occurring, high-affinity RNA ligands to human transforming growth factor beta2 (TGFbeta2). The CC oligonucleotide ligands were identified by the SELEX method (SELEX stands for Systemic Evolution of Ligands by Exponential Enrichment). The CC oligonucleotide ligands are useful in any process in which binding to CC TGFbeta2 is required. The ligands may be useful as pharmaceuticals, diagnostics, imaging agents and immunohistochemical reagents. The present CC sequence is an oligonucleotide used in the present invention.

XX

SQ Sequence 34 BP; 8 A; 6 C; 9 G; 0 T; 11 U; 0 Other;

Query Match 100.0%; Score 34; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.8e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGGUUUAUACAGAGUCUGUAGCUCUCC 34

Db 1 GGAGGUUUAUACAGAGUCUGUAGCUCUCC 34

RESULT 14

ID AAF90876 standard; RNA; 34 BP.

XX AAF90876;

XX 03-MAY-2001 (first entry)

XX NX22284 ligand variant #9.

XX Human; transforming growth factor beta2; TGFbeta2; SELEX; Systemic evolution of ligands by exponential enrichment; BB.

XX Homo sapiens.

XX WO200109156-A1.

XX 08-FEB-2001.

XX 26-JUL-2000; 2000WO-US020397.

XX PR 29-JUL-1999; 99US-00363939.

XX PA (NEXS-) NEXSTAR PHARM INC.

XX DR WPI; 2001-218217/22.

XX PT New RNA ligand to human transforming growth factor beta2, useful as pharmaceuticals, diagnostics and as immunohistochemical reagents.

XX

PS Claim 1; Page 78; 178pp; English.

XX The present invention relates to non-naturally occurring, high-affinity RNA ligands to human transforming growth factor beta2 (TGFbeta2). The CC oligonucleotide ligands were identified by the SELEX method (SELEX stands for Systemic Evolution of Ligands by Exponential Enrichment). The CC oligonucleotide ligands are useful in any process in which binding to CC TGFbeta2 is required. The ligands may be useful as pharmaceuticals, diagnostics, imaging agents and immunohistochemical reagents. The present CC sequence is an oligonucleotide used in the present invention.

XX

SQ Sequence 34 BP; 8 A; 6 C; 9 G; 0 T; 11 U; 0 Other;

Query Match 100.0%; Score 34; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.8e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGGUUUAUACAGAGUCUGUAGCUCUCC 34

Db 1 GGAGGUUUAUACAGAGUCUGUAGCUCUCC 34

RESULT 15

ID AAF90875 standard; RNA; 34 BP.

XX AAF90875;

XX 03-MAY-2001 (first entry)

XX NX22284 ligand variant #8.

XX Human; transforming growth factor beta2; TGFbeta2; SELEX; Systemic evolution of ligands by exponential enrichment; BB.

XX Homo sapiens.

XX WO200109156-A1.

XX
PD 08-FEB-2001.
XX
PP 26-JUL-2000; 2000WO-US020397.
XX
PR 29-JUL-1999; 99US-0363939.
XX
PA (NEXS-) NEYSTAR PHARM INC.
XX
PI Pagratis N, Lochrie M, Gold L;
XX
DR WPI; 2001-218217/22.
XX
PT New RNA ligand to human transforming growth factor beta2, useful as
PT pharmaceuticals, diagnostics and as immunohistochemical reagents.
XX
PS Claim 1; Page 78; 170pp; English.

CC The present invention relates to non-naturally occurring, high-affinity
CC RNA ligands to human transforming growth factor beta2 (TGFbeta2). The
CC Oligonucleotide ligands were identified by the SELEX method (SELEX stands
CC for Systemic Evolution of Ligands by Exponential Enrichment). The
CC Oligonucleotide ligands are useful in any process in which binding to
CC TGFbeta2 is required. The ligands may be useful as pharmaceuticals,
CC diagnostics, imaging agents and immunohistochemical reagents. The present
CC sequence is an oligonucleotide used in the present invention.
XX Sequence 34 BP; 8 A; 6 C; 9 G; 0 T; 11 U; 0 Other;
SQ

Query Match 100.0%; Score 34; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.8e-05; Mismatches 0;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 GAGGGGUAUUAGAGAGUCUGUUAAGCCGUAUCC 34
Db 1 GAGGGGUAUUAGAGAGUCUGUUAAGCCGUAUCC 34

Search completed: December 27, 2005, 15:06:36
Job time : 487 SECs

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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model
 Run on: December 27, 2005, 14:30:56 ; Search time 3758 Seconds
 (without alignments) 423.300 Million cell updates/sec

Title:

US-10-812-642-115

Perfect score:

34

Sequence:

1

gaggguaauacagacguacuacucc 34

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqB, 2339354128 residues

Total number of hits satisfying chosen parameters: 82156650

Maximum DB seq length: 0

Minimum DB seq length: 200000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database :

EST:
 1: gb_est1:
 2: gb_est2:
 3: gb_est3:
 4: gb_htc:
 5: gb_est:
 6: gb_est5:
 7: gb_est6:
 8: gb_est7:
 9: gb_g81:
 10: gb_g82:
 11: gb_g83:
 *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	22.2	65.3	732	7	CR420095
C 2	21.8	64.1	483	9	AQ46760
C 3	21.4	62.9	329	7	CR469204
C 4	21.4	62.9	730	8	CX909337
C 5	21.4	62.9	769	5	BUT47611
C 6	21.4	62.9	772	7	CR415821
C 7	21.4	62.9	1209	10	CL043735
C 8	21.2	62.4	509	9	AQ88713
C 9	21.2	62.4	734	9	BQ55939
C 10	21.2	62.4	900	10	DU036738
C 11	21.2	62.4	1163	8	DN704358
C 12	21.1	61.8	533	9	B2680408
C 13	21.1	61.8	632	10	CZ036446
C 14	21.1	61.8	679	11	CR157585
C 15	21.1	61.8	728	9	AQ258623
C 16	21.1	61.8	977	9	BZ394307
C 17	20.8	61.2	251	1	AV24404
C 18	20.8	61.2	281	5	BX335814
C 19	20.8	61.2	289	1	AA645178
C 20	20.8	61.2	319	8	CX200320
C 21	20.8	61.2	334	3	BW940310
C 22	20.8	61.2	381	9	AQ567614

OM nucleic - nucleic search, using sw model

Run on: December 27, 2005, 14:30:56 ; Search time 3758 Seconds

(without alignments) 423.300 Million cell updates/sec

Title:

US-10-812-642-115

Perfect score:

34

Sequence:

1

gaggguaauacagacguacuacucc 34

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Post-processing: Maximum Match 0%
Listing first 45 summaries

Database :

EST:
 1: gb_est1:
 2: gb_est2:
 3: gb_est3:
 4: gb_htc:
 5: gb_est:
 6: gb_est5:
 7: gb_est6:
 8: gb_est7:
 9: gb_g81:
 10: gb_g82:
 11: gb_g83:
 *

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C 4	21.4	62.9	730	8	CX909337
C 5	21.4	62.9	769	5	BUT47611
C 6	21.4	62.9	772	7	CR415821
C 7	21.4	62.9	1209	10	CL043735
C 8	21.2	62.4	509	9	AQ88713
C 9	21.2	62.4	734	9	BQ55939
C 10	21.2	62.4	900	10	DU036738
C 11	21.2	62.4	1163	8	DN704358
C 12	21.1	61.8	533	9	B2680408
C 13	21.1	61.8	632	10	CZ036446
C 14	21.1	61.8	679	11	CR157585
C 15	21.1	61.8	728	9	AQ258623
C 16	21.1	61.8	977	9	BZ394307
C 17	20.8	61.2	251	1	AV24404
C 18	20.8	61.2	281	5	BX335814
C 19	20.8	61.2	289	1	AA645178
C 20	20.8	61.2	319	8	CX200320
C 21	20.8	61.2	334	3	BW940310
C 22	20.8	61.2	381	9	AQ567614

OM nucleic - nucleic search, using sw model

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Title:

US-10-812-642-115

Perfect score:

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Sequence:

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gaggguaauacagacguacuacucc 34

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Searched: 41078325 seqB, 2339354128 residues

Total number of hits satisfying chosen parameters: 82156650

Maximum DB seq length: 0

Minimum DB seq length: 200000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database :

EST:
 1: gb_est1:
 2: gb_est2:
 3: gb_est3:
 4: gb_htc:
 5: gb_est:
 6: gb_est5:
 7: gb_est6:
 8: gb_est7:
 9: gb_g81:
 10: gb_g82:
 11: gb_g83:
 *

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C 5	21.4	62.9	769	5	BUT47611
C 6	21.4	62.9	772	7	CR415821
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C 8	21.2	62.4	509	9	AQ88713
C 9	21.2	62.4	734	9	BQ55939
C 10	21.2	62.4	900	10	DU036738
C 11	21.2	62.4	1163	8	DN704358
C 12	21.1	61.8	533	9	B2680408
C 13	21.1	61.8	632	10	CZ036446
C 14	21.1	61.8	679	11	CR157585
C 15	21.1	61.8	728	9	AQ258623
C 16	21.1	61.8	977	9	BZ394307
C 17	20.8	61.2	251	1	AV24404
C 18	20.8	61.2	281	5	BX335814
C 19	20.8	61.2	289	1	AA645178
C 20	20.8	61.2	319	8	CX200320
C 21	20.8	61.2	334	3	BW940310
C 22	20.8	61.2	381	9	AQ567614

OM nucleic - nucleic search, using sw model

Run on: December 27, 2005, 14:30:56 ; Search time 3758 Seconds

(without alignments) 423.300 Million cell updates/sec

Title:

US-10-812-642-115

Perfect score:

34

Sequence:

1

gaggguaauacagacguacuacucc 34

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqB, 2339354128 residues

Total number of hits satisfying chosen parameters: 82156650

Maximum DB seq length: 0

Minimum DB seq length: 200000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database :

EST:
 1: gb_est1:
 2: gb_est2:
 3: gb_est3:
 4: gb_htc:
 5: gb_est:
 6: gb_est5:
 7: gb_est6:
 8: gb_est7:
 9: gb_g81:
 10: gb_g82:
 11: gb_g83:
 *

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SUMMARIES

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C 4	21.4	62.9	730	8	CX909337
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C 6	21.4	62.9	772	7	CR415821
C 7	21.4	62.9	1209	10	CL043735
C 8	21.2	62.4	509	9	AQ88713
C 9	21.2	62.4	734	9	BQ55939
C 10	21.2	62.4	900	10	DU036738
C 11	21.2	62.4	1163	8	DN704358
C 12	21.1	61.8	533	9	B2680408
C 13	21.1	61.8	632	10	CZ036446
C 14	21.1	61.8	679	11	CR157585
C 15	21.1	61.8	728	9	AQ258623
C 16	21.1	61.8	977	9	BZ394307
C 17	20.8	61.2	251	1	AV24404
C 18	20.8	61.2	281	5	BX335814
C 19	20.8	61.2	289	1	AA645178
C 20	20.8	61.2	319	8	CX200320
C 21	20.8	61.2	334	3	BW940310
C 22	20.8	61.2	381	9	AQ567614

OM nucleic - nucleic search, using sw model

Run on: December 27, 2005, 14:30:56 ; Search time 3758 Seconds

(without alignments) 423.300 Million cell updates/sec

Title:

US-10-812-642-115

Perfect score:

34

Sequence:

1

gaggguaauacagacguacuacucc 34

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqB, 2339354128 residues

Total number of hits satisfying chosen parameters: 82156650

Maximum DB seq length: 0

Minimum DB seq length: 200000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database :

EST:
 1: gb_est1:
 2: gb_est2:
 3: gb_est3:
 4: gb_htc:
 5: gb_est:
 6: gb_est5:
 7: gb_est6:
 8: gb_est7:
 9: gb_g81:
 10: gb_g82:
 11: gb_g83:
 *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	22.2	65.3	732	7	CR420095
C 2	21.8	64.1			

QY	6	UUUUACAGAGUCGUUAUAGCUUACU	32	AUTHORS	Henrich,J., Hermanns,J., Kranz,H., Leibbert,R., Schlueter,T.,
LOCUS	AQ146760	483 bp	DNA	LINEAR	Heindl,M., Heil,O., Ebert,L., Neubert,P., Peters,M.,
DEFINITION	HS 2341-B2 D03 MR CIT Approved Human Genomic Sperm Library D				Schnette,D., Weindl,M., Heil,O., Ebert,L., Neubert,P., Peters,M.,
Db	182 TATTGAGAGCTGCTGACTA	156			Radelof,U., Schneider,D. and Korn,B.
ACCESSION	AQ146760			TITLE	Rat ArrayTAG cDNA
VERSION	AQ146760.1			JOURNAL	Unpublished (2004)
KEYWORDS	GSS.			COMMENT	Contact: Inge Arlart
ORGANISM	Homo sapiens				RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
	Homo sapiens (human)				Heubnerweg 6, D-1059 Berlin, Germany
REFERENCE	1 (bases 1 to 483)				Email: www.rzpd.de
AUTHORS	Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,				RZPD: lione63e08404 .
PUBMED	Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and				RZPLIB;
COMMENT	Hood,L.				Rat ArrayTAG cDNA
TITLE	Sequence-tagged connectors: A sequence approach to mapping and				http://www.rzpd.de/cgi-bin/product/showlib.pl.cgi/response?libNo=463
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)				Contact: Inge Arlart
PUBMED	10449164				Heubnerweg 6, D-1059 Berlin, Germany
COMMENT	Contact: Mahairas GG, Wallace JC, Hood L				Tel: +49 30 32639 100
	High Throughput Sequencing Center				Fax: +49 30 32639 111
FEATURES	University of Washington				www.rzpd.de
source	401 Queen Anne Avenue North, Seattle, WA 98109, USA				This clone is available royalty-free from RZPD;
	Tel: (206) 616-3618				contact RZPD (clone@rzpd.de) for further information. Seq primer:
	Fax: (206) 616-3887				RP: CAGGACACGCTATGC.
	Email: jwallace@u.washington.edu				Location/Qualifiers
	Sequence Tagged Connector				1..329
	Plate: 2241 Row: H Column: 6				/organism="Rattus norvegicus"
	Class: BAC ends				/mol_type="mRNA"
	High quality sequence stop: 483.				/db_xref="taxon:10116"
	Location/Qualifiers				/clone="LIONP63E08404"
	1..483				/lb_host="DH10B"
FEATURES	/organism="Homo sapiens"				/clone_lib="Rat pBlueScript Lion"
source	/mol_type="genomic DNA"				
	/db_xref="txon:9606"				
	/clone="Plate2241 Col=6 Row=H"				
	/sex="male"				
	/clone Lib="CIT Approved Human Genomic Sperm Library D"				
	/note="Organ: Sperm; Vector: pBlueBAC11; BAC Clones in				
	E. Coli DH10B"				
ORIGIN					
RESULT 3					
QY	5	GUUUACAGAGUCGUUAUAGCUU	29	DEFINITION	Query Match
Db	193	GTCATCTACAGAGCTGTTAGTGT	169	Best Local Similarity	62.9%
				Score	21.4;
				DB	7;
				Length	329;
				Matches	18;
				Conservative	7;
				Mismatches	6;
				Indels	0;
				Gaps	0;
FEATURES					
source					
RESULT 4					
QY	1	GGAGGAGGUAGAGUCGUUAUAGCUUACU	31	DEFINITION	Query Match
Db	195	GGAGAGTCTACAGAGCTGACAGCTCAC	165	Best Local Similarity	58.1%
				Score	21.4;
				DB	7;
				Length	329;
				Matches	18;
				Conservative	7;
				Mismatches	6;
				Indels	0;
				Gaps	0;
FEATURES					
source					
RESULT 5					
QY	1	GGAGGAGGUAGAGUCGUUAUAGCUUACU	31	DEFINITION	Query Match
Db	196	GGAGAGTCTACAGAGCTGACAGCTCAC	165	Best Local Similarity	58.1%
				Score	21.4;
				DB	7;
				Length	329;
				Matches	18;
				Conservative	7;
				Mismatches	6;
				Indels	0;
				Gaps	0;
FEATURES					
source					
RESULT 6					
QY	1	GGAGGAGGUAGAGUCGUUAUAGCUUACU	31	DEFINITION	Query Match
Db	197	GGAGAGTCTACAGAGCTGACAGCTCAC	165	Best Local Similarity	58.1%
				Score	21.4;
				DB	7;
				Length	329;
				Matches	18;
				Conservative	7;
				Mismatches	6;
				Indels	0;
				Gaps	0;
FEATURES					
source					
RESULT 7					
QY	1	GGAGGAGGUAGAGUCGUUAUAGCUUACU	31	DEFINITION	Query Match
Db	198	GGAGAGTCTACAGAGCTGACAGCTCAC	165	Best Local Similarity	58.1%
				Score	21.4;
				DB	7;
				Length	329;
				Matches	18;
				Conservative	7;
				Mismatches	6;
				Indels	0;
				Gaps	0;
FEATURES					
source					
RESULT 8					
QY	1	GGAGGAGGUAGAGUCGUUAUAGCUUACU	31	DEFINITION	Query Match
Db	199	GGAGAGTCTACAGAGCTGACAGCTCAC	165	Best Local Similarity	58.1%
				Score	21.4;
				DB	7;
				Length	329;
				Matches	18;
				Conservative	7;
				Mismatches	6;
				Indels	0;
				Gaps	0;
FEATURES					
source					
RESULT 9					
QY	1	GGAGGAGGUAGAGUCGUUAUAGCUUACU	31	DEFINITION	Query Match
Db	200	GGAGAGTCTACAGAGCTGACAGCTCAC	165	Best Local Similarity	58.1%
				Score	21.4;
				DB	7;
				Length	329;
				Matches	18;
				Conservative	7;
				Mismatches	6;
				Indels	0;
				Gaps	0;
FEATURES					
source					
RESULT 10					
QY	1	GGAGGAGGUAGAGUCGUUAUAGCUUACU	31	DEFINITION	Query Match
Db	201	GGAGAGTCTACAGAGCTGACAGCTCAC	165	Best Local Similarity	58.1%
				Score	21.4;
				DB	7;
				Length	329;
				Matches	18;
				Conservative	7;
				Mismatches	6;
				Indels	0;
				Gaps	0;
FEATURES					
source					
RESULT 11					
QY	1	GGAGGAGGUAGAGUCGUUAUAGCUUACU	31	DEFINITION	Query Match
Db	202	GGAGAGTCTACAGAGCTGACAGCTCAC	165	Best Local Similarity	58.1%
				Score	21.4;
				DB	7;
				Length	329;
				Matches	18;
				Conservative	7;
				Mismatches	6;
				Indels	0;
				Gaps	0;
FEATURES					
source					
RESULT 12					
QY	1	GGAGGAGGUAGAGUCGUUAUAGCUUACU	31	DEFINITION	Query Match
Db	203	GGAGAGTCTACAGAGCTGACAGCTCAC	165	Best Local Similarity	58.1%
				Score	21.4;
				DB	7;
				Length	329;
				Matches	18;
				Conservative	7;
				Mismatches	6;
				Indels	0;
				Gaps	0;
FEATURES					
source					
RESULT 13					
QY	1	GGAGGAGGUAGAGUCGUUAUAGCUUACU	31	DEFINITION	Query Match
Db	204	GGAGAGTCTACAGAGCTGACAGCTCAC	165	Best Local Similarity	58.1%
				Score	21.4;
				DB	7;
				Length	329;
				Matches	18;
				Conservative	7;
				Mismatches	6;
				Indels	0;
				Gaps	0;
FEATURES					
source					
RESULT 14					
QY	1	GGAGGAGGUAGAGUCGUUAUAGCUUACU	31	DEFINITION	Query Match
Db	205	GGAGAGTCTACAGAGCTGACAGCTCAC	165	Best Local Similarity	58.1%
				Score	21.4;
				DB	7;
				Length	329;
				Matches	18;
				Conservative	7;
				Mismatches	6;
				Indels	0;
				Gaps	0;
FEATURES					
source					
RESULT 15					
QY	1	GGAGGAGGUAGAGUCGUUAUAGCUUACU	31	DEFINITION	Query Match
Db	206	GGAGAGTCTACAGAGCTGACAGCTCAC	165	Best Local Similarity	58.1%
				Score	21.4;
				DB	7;
				Length	329;
				Matches	18;
				Conservative	7;
				Mismatches	6;
				Indels	0;
				Gaps	0;
FEATURES					
source					
RESULT 16					
QY	1	GGAGGAGGUAGAGUCGUUAUAGCUUACU	31	DEFINITION	Query Match
Db	207	GGAGAGTCTACAGAGCTGACAGCTCAC	165	Best Local Similarity	58.1%
				Score	21.4;
				DB	7;
				Length	329;
				Matches	18;
				Conservative	7;
				Mismatches	6;
				Indels	0;
				Gaps	0;
FEATURES					
source					
RESULT 17					
QY	1	GGAGGAGGUAGAGUCGUUAUAGCUUACU	31	DEFINITION	Query Match
Db	208	GGAGAGTCTACAGAGCTGACAGCTCAC	165	Best Local Similarity	58.1%
				Score	21.4;
				DB	7;
				Length	329;
				Matches	18;
				Conservative	7;
				Mismatches	6;
				Indels	0;
				Gaps	0;
FEATURES					
source					
RESULT 18					
QY	1	GGAGGAGGUAGAGUCGUUAUAGCUUACU	31	DEFINITION	Query Match
Db	209	GGAGAGTCTACAGAGCTGACAGCTCAC	165	Best Local Similarity	58.1%
				Score	21.4;
				DB	7;
				Length	329;
				Matches	18;
				Conservative	7;
				Mismatches	6;
				Indels	0;
				Gaps	0;
FEATURES</					

Matches	16;	Conservative	10;	Mismatches	8;	Indels	0;	Gaps	0;	JOURNAL	COMMENT
Qy	1	GAGGUUATACAGAGUCUGUAUAGCUGAACCC	34							Unpublished (2005)	Contact: Rod A. Wing
Db	952	GGTTTATTAAGAGCCCTGTTGCCTTACTCC	985							Arizona Genomics Institute	University of Arizona
RESULT	12									Forbes Building Room 303, Tucson, AZ 85721-0036, USA	Forbes Building Room 303, Tucson, AZ 85721-0036, USA
BZ680408	BZ680408	BZ680408	533 bp	DNA	linear	GSS 05-FEB-2003				Tel: 520 626 9595	
LOCUS		PUBGISTD ZM_0.6_1.0_KB								Fax: 520 621 1259	
DEFINITION		genomic survey sequence.								Email: rwing@genome.arizona.edu	
ACCESSION	BZ680408									PCR PrimerB	
VERSION	BZ680408.1	GI:28235276								FORWARD: TAA TAC GAC TCA CTA TAG GG	
KEYWORDS	GSS,									BACKWARD: CAC TCA TTA GGC ACC CCA	
SOURCE	zea mays									Plate: 0219 row: p column: 12	
ORGANISM	zea mays									Seq primer: CAC TCA TTA GGC ACC CCA	
TITLE	Maize Genomics Consortium									Class: BAC ends.	
JOURNAL										Location/Qualifiers	
COMMENT	Unpublished (2003)									1. . 632	
TIGR		Contact: Cathy Whitelaw								/organism="Oryza coarctata"	
	9712 Medical Center Drive, Rockville, MD 20850, USA									/mol_type="genomic DNA"	
	Tel: 301-838-5843									/db_xref="txaxon:7788"	
	Fax: 301-838-0208									/clone="OC_Ba0219P12"	
	Email: whitelaw@tigr.org									/tissue_type="leaves"	
	Seq primer: TF									/dev_stage="mature"	
	Class: sheared ends.									/lab_host="DHL0B"	
FEATURES	Location/Qualifiers									/clone lib="OC_Ba"	
source	1. . 533									/note="vector: PAGIBACI; site_1: HindIII; site_2: HindIII"	
ORIGIN											
Query Match	61.8%	Score 21;	DB 9;	Length 533;							
Best Local Similarity	48.3%	Pred. No. 5e+02;									
Matches	14;	Conservative	10;	Mismatches	5;	Indels	0;	Gaps	0;	RESULT	14
Qy	2	GAGGUUATACAGAGUCUGUAUAGCUGUA	30							CR157585	CR157585
Db	30	GAGGTGTTAGGAGCTGTGTTGCTGA	58							CR157585	CR157585
RESULT	13									CR157585	CR157585
C2336446	C2836446	C2836446	632 bp	DNA	linear	GSS 27-JUL-2005				CR157585	CR157585
LOCUS	OC_Ba0219P12.r	OC_Ba	Oryza coarctata	genomic clone	OC_Ba0219P12					Forward strand read from insert in 5' HPRR insertion targeting and	
DEFINITION	3', genomic	survey	sequence.							chromosome engineering clone MHPN356123, genomic survey sequence.	
ACCESSION	C2836446									CR157585	CR157585
VERSION	C2836446.1	GI:71289972								CR157585.1	CR157585.1
KEYWORDS	GSS,									GI:49936434	GI:49936434
SOURCE	Oryza coarctata (Portersea coarctata)										
ORGANISM	Oryza coarctata										
FEATURES	Location/Qualifiers										
source	1. . 679										
ORIGIN											
Query Match	61.8%	Score 21;	DB 11;	Length 679;							
Best Local Similarity	51.7%	Pred. No. 5.2e+02;									
Matches	15;	Conservative	9;	Mismatches	5;	Indels	0;	Gaps	0;	RESULT	13
Qy	6	UUAUACAGAGUCUGUAUAGCUGAACCC	34							PCR PrimerB	PCR PrimerB
Db	215	TTAGGACAACTGAGTGTGCTACTGC	243							FORWARD: TAA TAC GAC TCA CTA TAG GG	FORWARD: TAA TAC GAC TCA CTA TAG GG
REFERENCE	Ehrhardtdee, Oryzeae, Oryza.									BACKWARD: CAC TCA TTA GGC ACC CCA	BACKWARD: CAC TCA TTA GGC ACC CCA
AUTHORS	1 (bases 1 to 632)									Plate: 0219 row: p column: 12	Plate: 0219 row: p column: 12
TITLE	ONAP (Oryza Map Alignment Project) - Arizona Genomics Institute									Seq primer: CAC TCA TTA GGC ACC CCA	Seq primer: CAC TCA TTA GGC ACC CCA

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